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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 4.60064 seconds

(without alignments)
146.032 Million cell updates/sec

Title: US-09-887-853-6_COPY_222_230

Perfect score: 49

Sequence: 1 LQYAIFFPT 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------------------|-------------------|
| 1 | 49 | 100.0 | 107 | 3 | US-08-483-749A-26 | Sequence 26, Appl |
| 2 | 49 | 100.0 | 243 | 1 | US-08-133-804-6 | Sequence 6, Appl |
| 3 | 49 | 100.0 | 243 | 1 | US-08-461-838-6 | Sequence 6, Appl |
| 4 | 49 | 100.0 | 243 | 2 | US-08-461-386-6 | Sequence 6, Appl |
| 5 | 49 | 100.0 | 243 | 2 | US-08-356-786-4 | Sequence 4, Appl |
| 6 | 49 | 100.0 | 534 | 2 | US-08-356-786-10 | Sequence 10, Appl |
| 7 | 36 | 73.5 | 92 | 2 | US-08-273-146-47 | Sequence 47, Appl |
| 8 | 36 | 73.5 | 107 | 4 | US-09-648-067A-10 | Sequence 10, Appl |
| 9 | 36 | 73.5 | 107 | 4 | US-09-648-067A-12 | Sequence 12, Appl |
| 10 | 36 | 73.5 | 215 | 2 | US-08-737-129A-8 | Sequence 8, Appl |
| 11 | 36 | 73.5 | 355 | 3 | US-08-875-811-41 | Sequence 41, Appl |
| 12 | 36 | 73.5 | 355 | 3 | US-08-875-811-49 | Sequence 49, Appl |
| 13 | 36 | 73.5 | 355 | 3 | US-08-875-811-64 | Sequence 64, Appl |
| 14 | 36 | 73.5 | 358 | 3 | US-08-875-811-45 | Sequence 45, Appl |
| 15 | 36 | 73.5 | 358 | 3 | US-08-875-811-51 | Sequence 51, Appl |
| 16 | 36 | 73.5 | 360 | 3 | US-08-875-811-47 | Sequence 47, Appl |
| 17 | 36 | 73.5 | 379 | 3 | US-08-875-811-43 | Sequence 43, Appl |
| 18 | 35 | 71.4 | 92 | 2 | US-08-273-146-45 | Sequence 45, Appl |
| 19 | 35 | 71.4 | 92 | 2 | US-08-273-146-53 | Sequence 53, Appl |
| 20 | 35 | 71.4 | 107 | 3 | US-08-483-749A-12 | Sequence 12, Appl |
| 21 | 35 | 71.4 | 145 | 3 | US-09-096-244-2 | Sequence 2, Appl |
| 22 | 35 | 71.4 | 490 | 4 | US-09-270-767-42437 | Sequence 42437, A |
| 23 | 34 | 69.4 | 107 | 1 | US-07-634-278-50 | Sequence 50, Appl |
| 24 | 34 | 69.4 | 107 | 1 | US-07-634-278-51 | Sequence 51, Appl |
| 25 | 34 | 69.4 | 107 | 1 | US-08-477-728-50 | Sequence 50, Appl |
| 26 | 34 | 69.4 | 107 | 1 | US-08-477-728-51 | Sequence 51, Appl |
| 27 | 34 | 69.4 | 107 | 1 | US-08-474-040-50 | Sequence 50, Appl |

| | | | | | | |
|----|----|------|-----|---|----------------------|-------------------|
| 28 | 34 | 69.4 | 107 | 1 | US-08-474-040-51 | Sequence 51, Appl |
| 29 | 34 | 69.4 | 107 | 1 | US-08-487-200-50 | Sequence 50, Appl |
| 30 | 34 | 69.4 | 107 | 1 | US-08-487-200-51 | Sequence 51, Appl |
| 31 | 34 | 69.4 | 107 | 3 | US-08-484-537-50 | Sequence 50, Appl |
| 32 | 34 | 69.4 | 107 | 3 | US-08-484-537-51 | Sequence 51, Appl |
| 33 | 34 | 69.4 | 165 | 4 | US-09-248-796A-22117 | Sequence 22117, A |
| 34 | 34 | 69.4 | 313 | 4 | US-09-248-767-42252 | Sequence 42252, A |
| 35 | 34 | 69.4 | 322 | 4 | US-09-328-352-5739 | Sequence 5739, Ap |
| 36 | 33 | 67.3 | 106 | 1 | US-08-202-047-26 | Sequence 26, Appl |
| 37 | 33 | 67.3 | 106 | 3 | US-08-964-690-26 | Sequence 26, Appl |
| 38 | 33 | 67.3 | 156 | 4 | US-09-902-540-14530 | Sequence 14530, A |
| 39 | 33 | 67.3 | 345 | 4 | US-09-134-000C-5010 | Sequence 5010, Ap |
| 40 | 33 | 67.3 | 388 | 4 | US-09-560-761B-20 | Sequence 20, Appl |
| 41 | 32 | 65.3 | 95 | 2 | US-08-713-939A-72 | Sequence 72, Appl |
| 42 | 32 | 65.3 | 95 | 3 | US-09-036-579-72 | Sequence 72, Appl |
| 43 | 32 | 65.3 | 95 | 3 | US-09-550-374-72 | Sequence 72, Appl |
| 44 | 32 | 65.3 | 95 | 4 | US-09-943-906-72 | Sequence 72, Appl |
| 45 | 32 | 65.3 | 107 | 2 | US-08-290-592E-20 | Sequence 20, Appl |

ALIGNMENTS

RESULT 1
US-08-483-749A-26
Sequence 26, Application US/08483749A
Patent No. 6094561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESS: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-26
Query Match 100.0%; Score 49; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQYAIFFPT 9
|||
Db 89 LQYAIFFPT 97
RESULT 2

US-08-133-804-6
Sequence 6, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Houston, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 49; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYAIPT 9
DB 222 LOYAIPT 230

RESULT 3
US-08-461-838-6
Sequence 6, Application US/08461838
Patent No. 5753204
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-6

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-6

Query Match 100.0%; Score 49; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYAIPT 9
DB 222 LOYAIPT 230

RESULT 4
US-08-461-386-6
Sequence 6, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-6

Query Match 100.0%; Score 49; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
|||
Db 222 LOYALFPYT 230

RESULT 5
US-08-356-786-4
; Sequence 4, Application US/08356786
; Patent No. 587305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pletcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356.786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pletcher, Edmund R.
; REGISTRATION NUMBER: 27, 829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-4

Query Match 100.0%; Score 49; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
|||
Db 222 LOYALFPYT 230

RESULT 6
US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 587305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pletcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356.786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
REGISTRATION NUMBER: 27, 829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-10

Query Match 100.0%; Score 49; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
|||
Db 513 LOYALFPYT 521

RESULT 7
US-08-273-146-47
; Sequence 47, Application US/08273146
; Patent No. 585385
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-47

Query Match 73.5%; Score 36; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYAFPPYT 9
|||:||||
Db 81 LOYDERPPYT 89

RESULT 8
US-09-648-067A-10
Sequence 10, Application US/09648067A
Patent No. 6627196
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 107
TYPE: PRT
ORGANISM: Mus Musculus
US-09-648-067A-10

Query Match 73.5%; Score 36; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9
|||:||||
Db 90 QYIYPPYT 97

RESULT 9
US-09-648-067A-12
Sequence 12, Application US/09648067A
Patent No. 6627196
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 12
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized VL sequence
US-09-648-067A-12

Query Match 73.5%; Score 36; DB 4; Length 107;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAFPPYT 9
|||:||||
Db 90 QYIYPPYT 97

RESULT 10
US-08-737-129A-8
Sequence 8, Application US/08737129A
Patent No. 5885816
GENERAL INFORMATION:
APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,129A
FILING DATE: No. 5885816ember 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-129A-8

Query Match 73.5%; Score 36; DB 2; Length 215;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYAFPPYT 9
|||:||||
Db 89 LOYDERPPYT 97

RESULT 11
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-41

Query Match 73.5%; Score 36; DB 3; Length 355;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALPPT 9
DB 89 LQYDEFPPT 97

RESULT 12
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

Query Match 73.5%; Score 36; DB 3; Length 355;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALPPT 9
DB 89 LQYDEFPPT 97

RESULT 13
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997

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SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-875-811-45

Query Match
Best Local Similarity 73.5%; Score 36; DB 3; Length 358;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPPY 9
||| |||
Db 207 LQYDEFPY 215

RESULT 15
US-08-875-811-51
Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rydak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Farris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-875-811-51

Query Match
Best Local Similarity 73.5%; Score 36; DB 3; Length 358;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQYAFPPY 9
||| |||
Db 207 LQYDEFPY 215

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Tue Apr 5 08:00:43 2005

us-09-887-853-6_copy_222_230.rad

Page 7

Search completed: April 4, 2005, 16:00:52
Job time : 4.60064 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 3.57827 Seconds

(without alignments)
146.032 Million cell updates/sec

Title: US-09-887-853-6_COPY_183_189

Perfect score: 31

Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 31 | 100.0 | 92 | US-08-273-146-45 | Sequence 45, Appl |
| 2 | 31 | 100.0 | 92 | US-08-273-146-53 | Sequence 53, Appl |
| 3 | 31 | 100.0 | 107 | US-08-483-749A-26 | Sequence 26, Appl |
| 4 | 31 | 100.0 | 108 | US-09-726-218A-267 | Sequence 267, App |
| 5 | 31 | 100.0 | 109 | US-08-466-886-27 | Sequence 27, Appl |
| 6 | 31 | 100.0 | 109 | US-08-713-939A-74 | Sequence 74, Appl |
| 7 | 31 | 100.0 | 109 | US-08-469-617-27 | Sequence 27, Appl |
| 8 | 31 | 100.0 | 109 | US-09-036-579-74 | Sequence 74, Appl |
| 9 | 31 | 100.0 | 109 | US-09-550-374-74 | Sequence 74, Appl |
| 10 | 31 | 100.0 | 109 | US-09-943-906-74 | Sequence 74, Appl |
| 11 | 31 | 100.0 | 109 | US-08-469-630-27 | Sequence 27, Appl |
| 12 | 31 | 100.0 | 112 | US-09-627-218B-1 | Sequence 1, Appl |
| 13 | 31 | 100.0 | 243 | US-08-133-804-6 | Sequence 6, Appl |
| 14 | 31 | 100.0 | 243 | US-08-461-838-6 | Sequence 6, Appl |
| 15 | 31 | 100.0 | 243 | US-08-461-386-6 | Sequence 6, Appl |
| 16 | 31 | 100.0 | 243 | US-08-356-786-4 | Sequence 6, Appl |
| 17 | 31 | 100.0 | 534 | US-08-356-786-10 | Sequence 10, Appl |
| 18 | 31 | 100.0 | 694 | US-08-895-522-3 | Sequence 3, Appl |
| 19 | 31 | 100.0 | 694 | US-09-195-391-3 | Sequence 3, Appl |
| 20 | 31 | 100.0 | 747 | US-08-895-522-1 | Sequence 1, Appl |
| 21 | 31 | 100.0 | 747 | US-09-195-391-1 | Sequence 1, Appl |
| 22 | 28 | 90.3 | 109 | US-08-466-886-26 | Sequence 26, Appl |
| 23 | 28 | 90.3 | 109 | US-08-469-617-26 | Sequence 26, Appl |
| 24 | 28 | 90.3 | 109 | US-08-469-630-26 | Sequence 26, Appl |
| 25 | 28 | 90.3 | 111 | US-09-248-796A-20768 | Sequence 20768, A |
| 26 | 28 | 90.3 | 313 | US-09-134-000C-5794 | Sequence 5794, Ap |
| 27 | 28 | 90.3 | 439 | US-09-902-540-11372 | Sequence 11372, A |

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|----|----|------|------|---|----------------------|-------------------|
| 28 | 28 | 90.3 | 614 | 4 | US-09-540-236-2858 | Sequence 2858, Ap |
| 29 | 28 | 90.3 | 617 | 4 | US-09-328-352-6700 | Sequence 6700, Ap |
| 30 | 28 | 90.3 | 624 | 4 | US-09-252-992A-21625 | Sequence 21625, A |
| 31 | 28 | 90.3 | 744 | 4 | US-09-248-796A-20773 | Sequence 20773, A |
| 32 | 28 | 90.3 | 1307 | 1 | US-08-395-246C-2 | Sequence 2, Appl |
| 33 | 28 | 90.3 | 1334 | 2 | US-08-996-545-2 | Sequence 2, Appl |
| 34 | 28 | 90.3 | 1334 | 2 | US-09-328-320-2 | Sequence 2, Appl |
| 35 | 28 | 90.3 | 1334 | 4 | US-09-758-828-2 | Sequence 2, Appl |
| 36 | 28 | 90.3 | 1349 | 2 | US-08-612-734B-2 | Sequence 2, Appl |
| 37 | 28 | 90.3 | 1402 | 4 | US-09-711-619-9 | Sequence 9, Appl |
| 38 | 28 | 90.3 | 1408 | 1 | US-08-612-521-2 | Sequence 2, Appl |
| 39 | 27 | 87.1 | 105 | 3 | US-08-881-189B-13 | Sequence 13, Appl |
| 40 | 27 | 87.1 | 107 | 2 | US-08-888-366-14 | Sequence 14, Appl |
| 41 | 27 | 87.1 | 107 | 2 | US-08-888-366-20 | Sequence 20, Appl |
| 42 | 27 | 87.1 | 107 | 2 | US-08-888-366-26 | Sequence 26, Appl |
| 43 | 27 | 87.1 | 108 | 4 | US-09-270-767-35025 | Sequence 35025, A |
| 44 | 27 | 87.1 | 108 | 4 | US-09-270-767-50242 | Sequence 50242, A |
| 45 | 27 | 87.1 | 243 | 4 | US-09-134-000C-5004 | Sequence 5004, Ap |

ALIGNMENTS

RESULT 1
US-08-273-146-45
Sequence 45, Application US/08273146
Patent No. 5855865
GENERAL INFORMATION:
APPLICANT: Smith, Roger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
APPLICANT: Darsley, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kanten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The isolation and production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
Query Match 100.0%; Score 31; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 42 ATSSIDS 48

RESULT 2

US-08-273-146-53

; Sequence 53, Application US/08273146

; Patent No. 5855885

; GENERAL INFORMATION:

; APPLICANT: Smith, Rodger

; APPLICANT: McCafferty, John

; APPLICANT: Chiswell, David

; APPLICANT: Darsley, Michael J.

; APPLICANT: Fitzgerald, Kevin

; APPLICANT: Kenten, John H.

; APPLICANT: Martin, Mark T.

; APPLICANT: Tilmas, Richard C.

; APPLICANT: Williams, Richard O.

; TITLE OF INVENTION: The Isolation and Production of

; NUMBER OF INVENTION: Catalytic Antibodies using Phage Technology

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IGEN, Inc.

; STREET: 1530 East Jefferson St.

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20852

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/273,146

; FILING DATE: 14-JUL-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ryan, John W.

; REGISTRATION NUMBER: 33,771

; REFERENCE/DOCKET NUMBER: 09000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-984-8000

; TELEFAX: 301-230-0158

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 92 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-273-146-53

Query Match 100.0%; Score 31; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 42 ATSSIDS 48

RESULT 3

US-08-483-749A-26

; Sequence 26, Application US/08483749A

; Patent No. 6054561

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.

; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

; MOLECULES SPECIFIC FOR CANCER ANTIGENS

; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION

; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097

; CITY: EMERYVILLE

; STATE: CA

; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,749A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: SAVERIDE, PAUL B.

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0508,008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2585

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-483-749A-26

Query Match 100.0%; Score 31; DB 3; Length 107;

Best Local Similarity 100.0%; Pred. No. 8.2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 4

US-09-726-219A-267

; Sequence 267, Application US/09726219A

; Patent No. 6806079

; GENERAL INFORMATION:

; APPLICANT: Cambridge Antibody Technology

; APPLICANT: Cambridge Antibody Technology Limited

; APPLICANT: Medical Research Council

; APPLICANT: McCafferty, John

; APPLICANT: Pope, Anthony

; APPLICANT: Johnson, Kevin

; APPLICANT: Hoogenboom, Hendricus

; APPLICANT: Griffiths, Andrew

; APPLICANT: Jackson, Ronald

; APPLICANT: Holliger, Kasper

; APPLICANT: Marks, James

; APPLICANT: Clackson, Timothy

; APPLICANT: Chiswell, David

; APPLICANT: Winter, Gregory

; APPLICANT: Bonert, Timothy

; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

; FILE REFERENCE: 213839-00013

; CURRENT APPLICATION NUMBER: US/09/726,219A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: GB 9015198.6

; PRIOR FILING DATE: 1990-07-10

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9022845.3

; PRIOR FILING DATE: 1990-10-19

; PRIOR APPLICATION NUMBER: GB 9024503.6

; PRIOR FILING DATE: 1990-11-12

; PRIOR APPLICATION NUMBER: GB 9104744.9

PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 267
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain from clone M1F
US-09-726-219A-267

Query Match 100.0%; Score 31; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 5
US-08-466-886-27
Sequence 27, Application US/08466886
Patent No. 5776677
GENERAL INFORMATION:
APPLICANT: Teul, Lap-Chee
APPLICANT: Riordan, John R.
APPLICANT: Rommens, Johanna M.
APPLICANT: Kerem, Bat-Sheva
APPLICANT: Collins, Francis S.
APPLICANT: Iannuzzi, Michael C.
APPLICANT: Buckwald, Manuel
TITLE OF INVENTION: Cyclic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,886
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.001006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-466-886-27

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 99 ATSSIDS 105

RESULT 6
US-08-713-939A-74
Sequence 74, Application US/08713339A
Patent No. 5846533
GENERAL INFORMATION:
APPLICANT: Pusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PRP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 7
US-08-469-617-27
Sequence 27, Application US/08469617
Patent No. 6201107
GENERAL INFORMATION:
APPLICANT: Teul, Lap-Chee
APPLICANT: Riordan, John R.

```

APPLICANT: Rommens, Johanna M.
APPLICANT: Kerem, Bat-Sheva
APPLICANT: Collins, Francis S.
APPLICANT: Iannuzzi, Michael C.
APPLICANT: Drumm, Mitchell L.
APPLICANT: Buckwald, Manuel
TITLE OF INVENTION: Cystic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/469,617
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-469-617-27

Query Match      100.0%; Score 31; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
Db      99 ATSSIDS 105

RESULT 8
US-09-036-579-74
Sequence 74, Application US/09036579
Patent No. 6290954
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-74

Query Match      100.0%; Score 31; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
Db      50 ATSSIDS 56
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RESULT 9
US-09-550-374-74
Sequence 74, Application US/09550374
Patent No. 6372214
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-74

Query Match 100.0%; Score 31; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 10

US-09-943-906-74
Sequence 74, Application US/09943906
Patent No. 6562341
GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 11
US-08-469-630-27
Sequence 27, Application US/08469630
Patent No. 6730777

GENERAL INFORMATION:

APPLICANT: Tsui, Lap-Chee
APPLICANT: Riordan, John R.
APPLICANT: Rommens, Johanna M.
APPLICANT: Kerem, Bat-Sheva
APPLICANT: Collins, Francis S.
APPLICANT: Iannuzzi, Michael C.
APPLICANT: Drumm, Mitchell L.
APPLICANT: Buckwald, Manuel
TITLE OF INVENTION: Cyclic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,630
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-469-630-27

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 99 ATSSIDS 105

RESULT 12

US-09-627-218B-1
Sequence 1, Application US/09627218B
Patent No. 6537548
GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley
APPLICANT: Safar, Jiri
APPLICANT: Williamson, Anthony
APPLICANT: Burton, Dennis
TITLE OF INVENTION: Antibodies Specific for Ungulate PrP
FILE REFERENCE: UCAL-194
CURRENT APPLICATION NUMBER: US/09/627,218B
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 112
TYPE: PrP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized peptide

US-09-627-218B-1

Query Match 100.0%; Score 31; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|||||
Db 50 ATSSIDS 56

RESULT 13
US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:

APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-133-804-6

Query Match 100.0%; Score 31; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|||||
Db 183 ATSSIDS 189

RESULT 14
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:

APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For

TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-461-838-6

Query Match 100.0%; Score 31; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|||||
Db 183 ATSSIDS 189

RESULT 15
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:

APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7477
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 243 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-461-386-6

Query Match 100.0%; Score 31; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
 |||||
 DB 183 ATSSIDS 189

Search completed: April 4, 2005, 16:00:52
 Job time : 4.57827 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 5.623 Seconds
(without alignments)

146.032 Million cell updates/sec

Title: US-09-887-853-6_COPY_157_167

Perfect score: 53

Sequence: 1 RASODIGNSLT 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 53 | 100.0 | 107 | 3 | US-08-483-749A-26 |
| 2 | 53 | 100.0 | 243 | 1 | US-08-133-804-6 |
| 3 | 53 | 100.0 | 243 | 1 | US-08-461-838-6 |
| 4 | 53 | 100.0 | 243 | 2 | US-08-461-386-6 |
| 5 | 53 | 100.0 | 243 | 2 | US-08-356-786-4 |
| 6 | 53 | 100.0 | 534 | 2 | US-08-356-786-10 |
| 7 | 45 | 84.9 | 112 | 4 | US-09-627-218B-1 |
| 8 | 43 | 81.1 | 92 | 2 | US-08-273-146-45 |
| 9 | 43 | 81.1 | 92 | 2 | US-08-273-146-53 |
| 10 | 43 | 81.1 | 107 | 2 | US-08-888-366-14 |
| 11 | 43 | 81.1 | 107 | 2 | US-08-888-366-20 |
| 12 | 43 | 81.1 | 107 | 2 | US-08-888-366-26 |
| 13 | 43 | 81.1 | 108 | 4 | US-09-726-219A-267 |
| 14 | 43 | 81.1 | 109 | 2 | US-08-713-939A-74 |
| 15 | 43 | 81.1 | 109 | 3 | US-09-036-579-74 |
| 16 | 43 | 81.1 | 109 | 3 | US-09-550-374-74 |
| 17 | 43 | 81.1 | 109 | 4 | US-09-943-906-74 |
| 18 | 42 | 79.2 | 11 | 4 | US-09-155-106-4 |
| 19 | 42 | 79.2 | 108 | 4 | US-09-155-106-22 |
| 20 | 42 | 79.2 | 108 | 4 | US-09-155-106-23 |
| 21 | 42 | 79.2 | 108 | 4 | US-09-155-106-24 |
| 22 | 42 | 79.2 | 108 | 4 | US-09-155-106-28 |
| 23 | 42 | 79.2 | 108 | 4 | US-09-155-106-30 |
| 24 | 39 | 73.6 | 11 | 1 | US-07-942-245-497 |
| 25 | 39 | 73.6 | 31 | 3 | US-08-525-539A-3 |
| 26 | 39 | 73.6 | 95 | 2 | US-08-713-939A-72 |
| 27 | 39 | 73.6 | 95 | 3 | US-09-036-579-72 |

| | | | | | | |
|----|----|------|-----|---|-------------------|--------------------|
| 28 | 39 | 73.6 | 95 | 3 | US-09-550-374-72 | Sequence 72, Appl |
| 29 | 39 | 73.6 | 95 | 4 | US-09-943-906-72 | Sequence 72, Appl |
| 30 | 39 | 73.6 | 107 | 1 | US-08-436-463-20 | Sequence 20, Appl |
| 31 | 39 | 73.6 | 107 | 1 | US-08-107-669D-1 | Sequence 1, Appl |
| 32 | 39 | 73.6 | 107 | 1 | US-08-472-768A-1 | Sequence 1, Appl |
| 33 | 39 | 73.6 | 107 | 2 | US-08-477-531B-1 | Sequence 1, Appl |
| 34 | 39 | 73.6 | 107 | 2 | US-08-082-842A-1 | Sequence 1, Appl |
| 35 | 39 | 73.6 | 108 | 2 | US-08-378-939-26 | Sequence 26, Appl |
| 36 | 39 | 73.6 | 108 | 4 | US-09-232-230-27 | Sequence 27, Appl |
| 37 | 39 | 73.6 | 109 | 1 | US-07-942-245-4 | Sequence 4, Appl |
| 38 | 39 | 73.6 | 109 | 2 | US-08-713-939A-73 | Sequence 73, Appl |
| 39 | 39 | 73.6 | 109 | 3 | US-09-036-579-73 | Sequence 73, Appl |
| 40 | 39 | 73.6 | 109 | 3 | US-09-550-374-73 | Sequence 73, Appl |
| 41 | 39 | 73.6 | 109 | 4 | US-09-943-906-73 | Sequence 73, Appl |
| 42 | 38 | 71.7 | 11 | 4 | US-09-192-854-170 | Sequence 170, Appl |
| 43 | 38 | 71.7 | 106 | 4 | US-08-635-109-8 | Sequence 8, Appl |
| 44 | 38 | 71.7 | 106 | 4 | US-08-844-215-11 | Sequence 11, Appl |
| 45 | 37 | 69.8 | 96 | 4 | US-09-472-087-99 | Sequence 99, Appl |

ALIGNMENTS

```
RESULT 1
US-08-483-749A-26
; Sequence 26, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-749A-26

Query Match      100.0%; Score 53; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASODIGNSLT 11
      |||||
Db      24 RASODIGNSLT 34

RESULT 2
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US-08-133-804-6
Sequence 6, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 53; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
Db 157 RASQDIGNSLT 167

RESULT 3
US-08-461-838-6
Sequence 6, Application US/08461838
Patent No. 5753204
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-6

Query Match 100.0%; Score 53; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
Db 157 RASQDIGNSLT 167

RESULT 4
US-08-461-386-6
Sequence 6, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-6

Query Match 100.0%; Score 53; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
|||||
Db 157 RASODIGNSLT 167

RESULT 5
US-08-356-786-4
; Sequence 4, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7100
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-4

Query Match 100.0%; Score 53; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
|||||
Db 157 RASODIGNSLT 167

RESULT 6
US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7100
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-10

Query Match 100.0%; Score 53; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
|||||
Db 448 RASODIGNSLT 458

RESULT 7
US-09-627-218B-1
; Sequence 1, Application US/09627218B
; Patent No. 6537548
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley
; APPLICANT: Safar, Jiri
; APPLICANT: Williamson, Anthony
; APPLICANT: Burton, Dennis
; TITLE OF INVENTION: Antibodies Specific for Ungulate Prp
; FILE REFERENCE: UCAL-194
; CURRENT APPLICATION NUMBER: US/09/627,218B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PrP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide
US-09-627-218B-1

Query Match 84.9%; Score 45; DB 4; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
|||:|
Db 24 RASODIGNSL 33

RESULT 8

US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kerten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Williams, Richard C.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-273-146-45

Query Match 81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
|||:|
Db 16 RASODIGNSL 25

RESULT 9
US-08-273-146-53
; Sequence 53, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kerten, John H.

APPLICANT: Martin, Mark T.
APPLICANT: Tiltas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICANT: Martin, Mark T.
APPLICANT: Tiltas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-53

Query Match 81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
|||:|
Db 16 RASODIGNSL 25

RESULT 10
US-08-888-366-14
; Sequence 14, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Oswaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore

ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-14

Query Match 81.1%; Score 43; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 24 RASQDIGSSL 33

RESULT 11
US-08-888-366-20
Sequence 20, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Oswaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989

ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-20

Query Match 81.1%; Score 43; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 24 RASQDIGSSL 33

RESULT 12
US-08-888-366-26
Sequence 26, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Oswaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-26

Query Match
Best Local Similarity 90.0%; Score 43; DB 2; Length 107;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 13
US-09-726-219A-267
Sequence 267, Application US/09726219A

GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OR INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patent version 3.1
SEQ ID NO 267
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain from clone M1P
US-09-726-219A-267

Query Match
Best Local Similarity 90.0%; Score 43; DB 4; Length 108;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 14
US-08-713-939A-74

Sequence 74, Application US/08713939A
Patent No. 5846533
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match
Best Local Similarity 90.0%; Score 43; DB 2; Length 109;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 15
US-09-036-579-74
Sequence 74, Application US/09036579
Patent No. 6290954
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-74

Query Match 81.1%; Score 43; DB 3; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNSL 10
|||:|
Db 24 RASQDIGSSL 33

Search completed: April 4, 2005, 16:00:51
Job time : 6.623 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 3.06709 Seconds
 (without alignments)
 146.032 Million cell updates/sec

Title: US-09-887-853-6_COPY_99_104
 Perfect score: 34
 Sequence: 1 RFGPAY 6

Scoring table:
 BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA: *
 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
 3: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
 4: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
 5: /cgn2_6/ptodata/1/1aa/6D_COMB.pep:*
 6: /cgn2_6/ptodata/1/1aa/6E_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 34 | 100.0 | 115 | 3 | US-08-483-749A-24 |
| 2 | 34 | 100.0 | 243 | 1 | US-08-133-804-6 |
| 3 | 34 | 100.0 | 243 | 1 | US-08-461-838-6 |
| 4 | 34 | 100.0 | 243 | 2 | US-08-461-386-6 |
| 5 | 34 | 100.0 | 243 | 2 | US-08-356-786-4 |
| 6 | 34 | 100.0 | 453 | 2 | US-09-724-797-32 |
| 7 | 34 | 100.0 | 534 | 2 | US-08-356-786-10 |
| 8 | 30 | 88.2 | 571 | 4 | US-09-252-991A-28549 |
| 9 | 30 | 88.2 | 776 | 4 | US-09-165-396-3 |
| 10 | 30 | 88.2 | 858 | 4 | US-09-134-000C-5428 |
| 11 | 29 | 85.3 | 78 | 4 | US-09-248-796A-25202 |
| 12 | 29 | 85.3 | 351 | 4 | US-09-543-681A-6862 |
| 13 | 29 | 85.3 | 404 | 4 | US-09-153-599A-8 |
| 14 | 29 | 85.3 | 408 | 4 | US-09-328-352-6014 |
| 15 | 29 | 85.3 | 500 | 4 | US-09-248-796A-14502 |
| 16 | 29 | 85.3 | 514 | 3 | US-09-066-047-3 |
| 17 | 29 | 85.3 | 594 | 3 | US-08-581-148C-14 |
| 18 | 29 | 85.3 | 885 | 3 | US-09-107-532A-5104 |
| 19 | 28 | 82.4 | 60 | 4 | US-09-248-796A-25174 |
| 20 | 28 | 82.4 | 83 | 4 | US-09-270-767-35045 |
| 21 | 28 | 82.4 | 83 | 4 | US-09-252-991A-50262 |
| 22 | 28 | 82.4 | 138 | 4 | US-09-252-991A-17424 |
| 23 | 28 | 82.4 | 172 | 1 | US-07-949-812-9 |
| 24 | 28 | 82.4 | 172 | 2 | US-08-943-814-2 |
| 25 | 28 | 82.4 | 173 | 2 | US-08-702-703-2 |
| 26 | 28 | 82.4 | 173 | 2 | US-08-943-814-10 |
| 27 | 28 | 82.4 | 332 | 4 | US-09-107-433-3771 |

| | | | | | | |
|----|----|------|-----|---|----------------------|--------------------|
| 28 | 28 | 82.4 | 396 | 3 | US-09-134-001C-4580 | Sequence 4580, Ap |
| 29 | 28 | 82.4 | 409 | 4 | US-09-583-110-3394 | Sequence 3394, Ap |
| 30 | 28 | 82.4 | 451 | 4 | US-09-902-540-15200 | Sequence 15200, A |
| 31 | 28 | 82.4 | 689 | 4 | US-09-902-540-14254 | Sequence 14254, A |
| 32 | 28 | 82.4 | 815 | 4 | US-09-489-039A-12469 | Sequence 12469, A |
| 33 | 28 | 82.4 | 824 | 4 | US-09-252-991A-6425 | Sequence 18601, A |
| 34 | 28 | 82.4 | 827 | 4 | US-09-543-681A-6425 | Sequence 6425, Ap |
| 35 | 27 | 79.4 | 68 | 4 | US-09-328-352-60066 | Sequence 60066, Ap |
| 36 | 27 | 79.4 | 138 | 4 | US-09-328-352-8007 | Sequence 8007, Ap |
| 37 | 27 | 79.4 | 149 | 4 | US-09-543-681A-8072 | Sequence 8072, Ap |
| 38 | 27 | 79.4 | 154 | 4 | US-09-583-110-5042 | Sequence 5042, Ap |
| 39 | 27 | 79.4 | 158 | 4 | US-09-107-433-4659 | Sequence 4659, Ap |
| 40 | 27 | 79.4 | 178 | 4 | US-09-328-352-7054 | Sequence 7054, Ap |
| 41 | 27 | 79.4 | 211 | 4 | US-09-489-039A-8497 | Sequence 8497, Ap |
| 42 | 27 | 79.4 | 215 | 4 | US-09-902-540-10983 | Sequence 10983, A |
| 43 | 27 | 79.4 | 262 | 4 | US-09-949-016-10824 | Sequence 10824, A |
| 44 | 27 | 79.4 | 262 | 4 | US-09-949-016-10825 | Sequence 10825, A |
| 45 | 27 | 79.4 | 262 | 4 | US-09-949-016-10826 | Sequence 10826, A |

ALIGNMENTS

RESULT 1
 US-08-483-749A-24
 Sequence 24, Application US/08483749A
 Patent No. 6054561
 GENERAL INFORMATION:
 APPLICANT: RING, DAVID B.
 TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 TITLE OR INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESSES:
 ADDRESS: CHIRON CORPORATION
 STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 CITY: EMERYVILLE
 STATE: CA
 COUNTRY: USA
 ZIP: 94662-8097
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,749A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: SAVERIDE, PAUL B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0508.008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2585
 TELEFAX: (510) 655-3542
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-749A-24

Query Match
 Best Local Similarity 100.0%; Score 34; DB 3; Length 115;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RFGPAY 6
 |||||
 Db 99 RFGPAY 104

RESULT 2

US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-133-804-6
Query Match 100.0%; Score 34; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RFGFAY 6
Db 99 RFGFAY 104
RESULT 3
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-838-6

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-838-6

Query Match 100.0%; Score 34; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGFAY 6
Db 99 RFGFAY 104

RESULT 4
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-386-6

Query Match 100.0%; Score 34; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6
 Db 99 RRGPAY 104

RESULT 5
 US-08-356-786-4
 ; Sequence 4, Application US/08356786
 ; Patent No. 5877305

GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Houston, L. L.
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 TITLE OF INVENTION: Marker
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 REGISTRATION NUMBER: 27,829
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 243 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-356-786-4

Query Match 100.0%; Score 34; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6
 Db 99 RRGPAY 104

RESULT 6
 US-09-724-797-32
 ; Sequence 32, Application US/09724797
 ; Patent No. 6733998

GENERAL INFORMATION:
 APPLICANT: Jon S. THORSON
 TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
 TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
 TITLE OF INVENTION: CALICHEMICIN AND SELF-RESISTANCE THERETO

FILE REFERENCE: 2653-40
 CURRENT APPLICATION NUMBER: US/09/724,797
 CURRENT FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 60/111,325
 PRIOR FILING DATE: 1998-12-07
 NUMBER OF SEQ ID NOS: 95
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 32
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Bacteria
 US-09-724-797-32

Query Match 100.0%; Score 34; DB 4; Length 453;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6
 Db 443 RRGPAY 448

RESULT 7
 US-08-356-786-10
 ; Sequence 10, Application US/08356786
 ; Patent No. 5877305

GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Houston, L. L.
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 TITLE OF INVENTION: Marker
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 REGISTRATION NUMBER: 27,829
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 534 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-356-786-10

Query Match 100.0%; Score 34; DB 2; Length 534;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRGPAY 6
 Db 443 RRGPAY 448

RESULT 8
 US-09-724-797-32
 ; Sequence 32, Application US/09724797
 ; Patent No. 6733998

GENERAL INFORMATION:
 APPLICANT: Jon S. THORSON
 TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
 TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
 TITLE OF INVENTION: CALICHEMICIN AND SELF-RESISTANCE THERETO

Db 388 RRGFAY 393

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RESULT 8
US-09-252-991A-28549
; Sequence 28549, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28549
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28549
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Query Match 88.2%; Score 30; DB 4; Length 571;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 348 RRGFAY 353

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RESULT 9
US-09-165-396-3
; Sequence 3, Application US/09165396
; Patent No. 6441134
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY W.
; APPLICANT: LUBKOWITZ, MARK A.
; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE
; FILE REFERENCE: 372.6520P
; CURRENT APPLICATION NUMBER: US/09/165,396
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: PCT/US98/02332
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/037,859
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 776
; TYPE: PRT
; ORGANISM: S. pombe
US-09-165-396-3
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Query Match 88.2%; Score 30; DB 4; Length 776;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 195 RRGFAY 200

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RESULT 10
US-09-134-000C-5428
; Sequence 5428, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
```

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5428
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5428
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Query Match 88.2%; Score 30; DB 4; Length 858;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
Db 139 QRGFAY 144

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RESULT 11
US-09-248-796A-25202
; Sequence 25202, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25202
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25202
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Query Match 85.3%; Score 29; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRGFAY 6
Db 74 RRGFAY 78

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RESULT 12
US-09-543-681A-6862
; Sequence 6862, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6862
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Proteus mirabilis
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US-09-543-681A-6862

Query Match 85.3%; Score 29; DB 4; Length 351;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGFAY 6
 DB 243 RGFAY 248

RESULT 13

US-09-153-599A-8
 Sequence 8, Application US/09153599A
 Patent No. 6420177

GENERAL INFORMATION:
 APPLICANT: Weber, J. Mark
 APPLICANT: Lau, B. Minh
 TITLE OF INVENTION: Method for Strain Improvement of
 TITLE OF INVENTION: Erythromycin Producing Bacterium
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Rokey, Minamow & Katz, Ltd.
 STREET: 180 N. Steetson Avenue, 2 Prudential Plaza
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/153,599A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V.
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: FER2159P0041US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 404 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-153-599A-8

Query Match 85.3%; Score 29; DB 4; Length 404;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGFAY 6
 DB 49 RGFAY 54

RESULT 14

US-09-328-352-6014
 Sequence 6014, Application US/09328352
 Patent No. 6562958

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6014
 LENGTH: 408
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-6014

Query Match 85.3%; Score 29; DB 4; Length 408;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGFAY 6
 DB 317 RGFAY 321

RESULT 15

US-09-248-796A-14502
 Sequence 14502, Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:
 APPLICANT: Keith Weinstein et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 14502
 LENGTH: 500
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-14502

Query Match 85.3%; Score 29; DB 4; Length 500;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGFAY 6
 DB 275 RGFAY 280

Search completed: April 4, 2005, 16:00:53
 Job time : 4.06709 secs

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US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 97; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 4,4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGOSTYADDFKE 17
DB 50 WINTYGOSTYADDFKE 66

RESULT 3
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-6

Query Match 100.0%; Score 97; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 4,4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGOSTYADDFKE 17
DB 50 WINTYGOSTYADDFKE 66

RESULT 4
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-386-6

Query Match 100.0%; Score 97; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17
|||||
DB 50 WINTYGSTYADDFKE 66

RESULT 5

US-08-356-786-4
; Sequence 4, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Opertmann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-4

Query Match 100.0%; Score 97; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17
|||||
DB 50 WINTYGSTYADDFKE 66

RESULT 6

US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Opertmann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-10

Query Match 100.0%; Score 97; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGSTYADDFKE 17
|||||
DB 339 WINTYGSTYADDFKE 355

RESULT 7

US-08-875-811-53
; Sequence 53, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fairis, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-53

Query Match          91.8%; Score 89; DB 3; Length 365;
Best Local Similarity 93.8%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WINTYTGQSTYADDFK 16
Db      168 WINTYTGSTYADDFK 183

RESULT 8
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fairis, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
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```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-55

Query Match          91.8%; Score 89; DB 3; Length 366;
Best Local Similarity 93.8%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WINTYTGQSTYADDFK 16
Db      51 WINTYTGSTYADDFK 66

RESULT 9
US-08-279-772A-6
; Sequence 6, Application US/08279772A
; Patent No. 6080560
; GENERAL INFORMATION:
; APPLICANT: Russell, David R
; APPLICANT: Fuller, James T
; TITLE OF INVENTION: Method for Producing Antibodies in Plant
; TITLE OF INVENTION: Cells
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Quarles and Brady
; STREET: PO Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: United States of America
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,772A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 11-229-9097-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-279-772A-6

Query Match          89.7%; Score 87; DB 3; Length 252;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 WINTYTGQSTYADDFK 16
Db      180 WINTYTGQPTYADDFK 195

RESULT 10
US-08-902-486-9
; Sequence 9, Application US/08902486
; Patent No. 6140075
; GENERAL INFORMATION:
; APPLICANT: Russell, David R.
; APPLICANT: Fuller, James T.
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
; TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
```

```

/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles & Brady
/ STREET: 1 South Pluckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/902,486
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 670513.90261
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 252 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-902-486-9

Query Match      89.7%; Score 87; DB 3; Length 252;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WINTYGOSTYADDFK 16
DB      180 WINTYGOSTYADDFK 195

RESULT 11
US-09-485-737B-102
/ Sequence 102, Application US/09485737B
/ Patent No. 6350860
/ GENERAL INFORMATION:
/ APPLICANT: Buyse, Marie-Ange
/ APPLICANT: Sablon, Erwin
/ TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
/ TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
/ FILE REFERENCE: INNS:015
/ CURRENT APPLICATION NUMBER: US/09/485,737B
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: PCT/EP 98/05165
/ PRIOR FILING DATE: 1998-08-14
/ PRIOR APPLICATION NUMBER: EPO 98870139.7
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: EPO 97870122.5
/ PRIOR FILING DATE: 1997-08-18
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 102
/ LENGTH: 230
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC
/
US-09-485-737B-102

Query Match      87.6%; Score 85; DB 3; Length 230;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 WINTYGOSTYADDFK 16
DB      50 WINTYGESTYVDDFK 65

RESULT 12
US-10-071-485-102
/ Sequence 102, Application US/10071485
/ Patent No. 6830752
/ GENERAL INFORMATION:
/ APPLICANT: Buyse, Marie-Ange
/ APPLICANT: Sablon, Erwin
/ TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
/ TITLE OF INVENTION: SHOCK,
/ TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
/ FILE REFERENCE: INNS:015
/ CURRENT APPLICATION NUMBER: US/10/071,485
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 09/485,737
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: PCT/EP 98/05165
/ PRIOR FILING DATE: 1998-08-14
/ PRIOR APPLICATION NUMBER: EPO 98870139.7
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: EPO 97870122.5
/ PRIOR FILING DATE: 1997-08-18
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 102
/ LENGTH: 230
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC
/
US-10-071-485-102

Query Match      87.6%; Score 85; DB 4; Length 230;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WINTYGOSTYADDFK 16
DB      50 WINTYGESTYVDDFK 65

RESULT 13
US-09-485-737B-93
/ Sequence 93, Application US/09485737B
/ Patent No. 6350860
/ GENERAL INFORMATION:
/ APPLICANT: Buyse, Marie-Ange
/ APPLICANT: Sablon, Erwin
/ TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
/ TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
/ FILE REFERENCE: INNS:015
/ CURRENT APPLICATION NUMBER: US/09/485,737B
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: PCT/EP 98/05165
/ PRIOR FILING DATE: 1998-08-14
/ PRIOR APPLICATION NUMBER: EPO 98870139.7
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: EPO 97870122.5
/ PRIOR FILING DATE: 1997-08-18
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 93
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC
/
US-09-485-737B-93
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Query Match 87.6%; Score 85; DB 3; Length 235;
Best Local Similarity 87.5%; Pred. No. 2.8e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 50 WINTYTGESTYVDDFK 65

RESULT 14

US-10-071-485-93
; Sequence 93, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 93
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-93

Query Match 87.6%; Score 85; DB 4; Length 235;
Best Local Similarity 87.5%; Pred. No. 2.8e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 50 WINTYTGESTYVDDFK 65

RESULT 15

US-09-485-737B-91
; Sequence 91, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-91

Query Match 87.6%; Score 85; DB 3; Length 240;
Best Local Similarity 87.5%; Pred. No. 2.8e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 50 WINTYTGESTYVDDFK 65

Search completed: April 4, 2005, 16:00:50
Job time : 8.6901 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 2.55591 Seconds

(without alignments)
146.032 Million cell updates/sec

Title: US-09-887-853-6_COPY_31_35

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB | ID | Description |
|------------|-------|-------|--------------|----|---------------------|--------------------|
| 1 | 30 | 100.0 | 5 | 3 | US-08-783-853A-8 | Sequence 8, Appl |
| 2 | 30 | 100.0 | 5 | 3 | US-09-344-050-8 | Sequence 8, Appl |
| 3 | 30 | 100.0 | 74 | 3 | US-09-134-001C-3503 | Sequence 3503, Ap |
| 4 | 30 | 100.0 | 92 | 3 | US-08-783-853A-84 | Sequence 84, Appl |
| 5 | 30 | 100.0 | 92 | 3 | US-09-344-050-84 | Sequence 84, Appl |
| 6 | 30 | 100.0 | 112 | 3 | US-08-783-853A-20 | Sequence 20, Appl |
| 7 | 30 | 100.0 | 112 | 3 | US-09-344-050-20 | Sequence 20, Appl |
| 8 | 30 | 100.0 | 115 | 3 | US-08-483-749A-24 | Sequence 24, Appl |
| 9 | 30 | 100.0 | 117 | 1 | US-08-249-013-6 | Sequence 6, Appl |
| 10 | 30 | 100.0 | 117 | 2 | US-08-886-863-6 | Sequence 6, Appl |
| 11 | 30 | 100.0 | 117 | 3 | US-09-175-229-6 | Sequence 6, Appl |
| 12 | 30 | 100.0 | 117 | 5 | PCT-US95-06764-6 | Sequence 6, Appl |
| 13 | 30 | 100.0 | 118 | 1 | US-08-425-336-124 | Sequence 124, Appl |
| 14 | 30 | 100.0 | 118 | 1 | US-08-425-336-126 | Sequence 126, App |
| 15 | 30 | 100.0 | 118 | 1 | US-08-488-113B-124 | Sequence 124, App |
| 16 | 30 | 100.0 | 118 | 1 | US-08-488-113B-126 | Sequence 126, App |
| 17 | 30 | 100.0 | 118 | 1 | US-08-477-484B-124 | Sequence 124, App |
| 18 | 30 | 100.0 | 118 | 1 | US-08-477-484B-126 | Sequence 126, App |
| 19 | 30 | 100.0 | 118 | 1 | US-08-107-669D-28 | Sequence 28, Appl |
| 20 | 30 | 100.0 | 118 | 1 | US-08-107-669D-29 | Sequence 29, Appl |
| 21 | 30 | 100.0 | 118 | 1 | US-08-107-669D-66 | Sequence 66, Appl |
| 22 | 30 | 100.0 | 118 | 1 | US-08-107-669D-67 | Sequence 67, Appl |
| 23 | 30 | 100.0 | 118 | 1 | US-08-472-788A-28 | Sequence 28, Appl |
| 24 | 30 | 100.0 | 118 | 1 | US-08-472-788A-29 | Sequence 29, Appl |
| 25 | 30 | 100.0 | 118 | 1 | US-08-472-788A-68 | Sequence 88, Appl |
| 26 | 30 | 100.0 | 118 | 1 | US-08-472-788A-89 | Sequence 89, Appl |
| 27 | 30 | 100.0 | 118 | 2 | US-08-477-531B-28 | Sequence 28, Appl |

| | | | | | | |
|----|----|-------|-----|---|-------------------|-------------------|
| 28 | 30 | 100.0 | 118 | 2 | US-08-477-531B-29 | Sequence 29, Appl |
| 29 | 30 | 100.0 | 118 | 2 | US-08-477-531B-66 | Sequence 66, Appl |
| 30 | 30 | 100.0 | 118 | 2 | US-08-477-531B-67 | Sequence 67, Appl |
| 31 | 30 | 100.0 | 118 | 2 | US-08-646-360-124 | Sequence 124, App |
| 32 | 30 | 100.0 | 118 | 2 | US-08-646-360-126 | Sequence 126, App |
| 33 | 30 | 100.0 | 118 | 2 | US-08-082-842A-28 | Sequence 28, Appl |
| 34 | 30 | 100.0 | 118 | 2 | US-08-082-842A-29 | Sequence 29, Appl |
| 35 | 30 | 100.0 | 118 | 2 | US-08-082-842A-88 | Sequence 88, Appl |
| 36 | 30 | 100.0 | 118 | 2 | US-08-082-842A-89 | Sequence 89, Appl |
| 37 | 30 | 100.0 | 118 | 3 | US-08-839-765-124 | Sequence 124, App |
| 38 | 30 | 100.0 | 118 | 3 | US-08-839-765-126 | Sequence 126, App |
| 39 | 30 | 100.0 | 118 | 3 | US-09-136-389-124 | Sequence 124, App |
| 40 | 30 | 100.0 | 118 | 3 | US-09-136-389-126 | Sequence 126, App |
| 41 | 30 | 100.0 | 118 | 3 | US-09-610-838-124 | Sequence 124, App |
| 42 | 30 | 100.0 | 118 | 3 | US-09-610-838-126 | Sequence 126, App |
| 43 | 30 | 100.0 | 118 | 4 | US-09-440-781-96 | Sequence 96, Appl |
| 44 | 30 | 100.0 | 118 | 4 | US-09-711-485-124 | Sequence 124, App |
| 45 | 30 | 100.0 | 118 | 4 | US-09-711-485-126 | Sequence 126, App |

ALIGNMENTS

RESULT 1
US-08-783-853A-8
Sequence 8, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783, 853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33, 833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-8

Query Match 100.0%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 2
US-09-344-050-8
Sequence 8, Application US/09344050
Patent No. 6391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-344-050-8
Query Match 100.0%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 3
US-09-134-001C-3503
Sequence 3503, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3503
LENGTH: 74
TYPE: prf
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3503

Query Match 100.0%; Score 30; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 4 NYGMN 8

RESULT 4
US-08-783-853A-84
Sequence 84, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-783-853A-84

Query Match 100.0%; Score 30; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5
Db 8 NYGMN 12

RESULT 5
US-09-344-050-84
Sequence 84, Application US/09344050
Patent No. 6391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-344-050-84

Query Match 100.0%; Score 30; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5
Db 8 NYGMN 12

RESULT 6
US-08-783-853A-20
Sequence 20, Application US/08783853A
Patent No. 6009091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-20

Query Match 100.0%; Score 30; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
Db 28 NYGMN 32

RESULT 7
US-09-344-050-20
Sequence 20, Application US/09344050
Patent No. 6391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padiam, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-344-050-20

Query Match 100.0%; Score 30; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
Db 28 NYGMN 32

RESULT 8
US-08-483-749A-24
Sequence 24, Application US/08483749A
Patent No. 6054561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-24

Query Match 100.0%; Score 30; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
Db 31 NYGMN 35

RESULT 9
US-08-249-013-6
Sequence 6, Application US/08249013
Patent No. 5643754
GENERAL INFORMATION:
APPLICANT: Haake, David A.
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,013
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tumarkin Ph.D., Lisa A.,
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: lufa
FEATURE:
NAME/KEY: Protein
LOCATION: 1..117
US-08-249-013-6

Query Match 100.0%; Score 30; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 22 NYGMN 26

RESULT 10
US-08-886-863-6
Sequence 6, Application US/08886863
Patent No. 5824321
GENERAL INFORMATION:
APPLICANT: Haake, David A.
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,863
FILING DATE: 01-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,013
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tumarkin Ph.D., Lisa A.,
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: lufa
FEATURE:
NAME/KEY: Protein
LOCATION: 1..117
US-08-886-863-6

Query Match 100.0%; Score 30; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 22 NYGMN 26

RESULT 11
US-09-175-229-6
Sequence 6, Application US/09175229
Patent No. 6309641
GENERAL INFORMATION:
APPLICANT: Haake, David A.
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/175,229
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,013
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tumarkin Ph.D., Lisa A.,
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: lufa
FEATURE:
NAME/KEY: Protein
LOCATION: 1..117
US-09-175-229-6

Query Match 100.0%; Score 30; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 22 NYGMN 26

RESULT 12

PCT-US95-06764-6
Sequence 6, Application PC/TUS9506764

GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla
STATE: California

COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06764
FILING DATE: 25-MAY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: FD3602
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
IMMEDIATE SOURCE:

CLONE: lnta
FEATURE:

NAME/KEY: Protein
LOCATION: 1..117

PCT-US95-06764-6

Query Match 100.0%; Score 30; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5
Db 22 NYGMN 26

RESULT 13

US-08-425-336-124
Sequence 124, Application US/08425336

Patent No. 5621083
GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691

FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-425-336-124
Query Match 100.0%; Score 30; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5
Db 31 NYGMN 35

RESULT 14

US-08-425-336-126
Sequence 126, Application US/08425336

Patent No. 5621083
GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-126

Query Match 100.0%; Score 30; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 31 NYGMN 35

RESULT 15
US-08-488-113B-124
Sequence 124, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-124

Query Match 100.0%; Score 30; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 31 NYGMN 35

Search completed: April 4, 2005, 16:00:50
Job time : 3.55591 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 124.217 seconds
(without alignments)
146.032 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EIQLVQSGPELKKPGETVKI.....VAIFPYTGGTINLEIKRAD 243

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1 | 1258 | 100.0 | 243 | 1 | US-08-133-804-6 Sequence 6, Appl1 |
| 2 | 1258 | 100.0 | 243 | 1 | US-08-461-838-6 Sequence 6, Appl1 |
| 3 | 1258 | 100.0 | 243 | 2 | US-08-461-386-6 Sequence 6, Appl1 |
| 4 | 1258 | 100.0 | 243 | 2 | US-08-356-786-4 Sequence 4, Appl1 |
| 5 | 1214 | 96.5 | 534 | 2 | US-08-356-786-10 Sequence 10, Appl1 |
| 6 | 914 | 72.7 | 250 | 1 | US-08-133-804-2 Sequence 2, Appl1 |
| 7 | 914 | 72.7 | 250 | 1 | US-08-461-184-8 Sequence 8, Appl1 |
| 8 | 914 | 72.7 | 250 | 1 | US-08-463-675-8 Sequence 8, Appl1 |
| 9 | 914 | 72.7 | 250 | 1 | US-08-464-589-8 Sequence 8, Appl1 |
| 10 | 914 | 72.7 | 250 | 1 | US-08-461-838-2 Sequence 2, Appl1 |
| 11 | 914 | 72.7 | 250 | 2 | US-08-461-386-2 Sequence 2, Appl1 |
| 12 | 891 | 70.8 | 622 | 2 | US-08-356-786-16 Sequence 16, Appl1 |
| 13 | 827 | 65.7 | 240 | 1 | US-08-488-113B-148 Sequence 148, App |
| 14 | 827 | 65.7 | 240 | 1 | US-08-477-484B-148 Sequence 148, App |
| 15 | 827 | 65.7 | 240 | 2 | US-08-646-360-148 Sequence 148, App |
| 16 | 827 | 65.7 | 240 | 3 | US-08-839-765-148 Sequence 148, App |
| 17 | 827 | 65.7 | 240 | 3 | US-09-136-389-148 Sequence 148, App |
| 18 | 827 | 65.7 | 240 | 3 | US-09-610-838-148 Sequence 148, App |
| 19 | 827 | 65.7 | 240 | 4 | US-09-711-485-148 Sequence 148, App |
| 20 | 823.5 | 65.5 | 530 | 4 | US-08-840-713-2 Sequence 2, Appl1 |
| 21 | 823.5 | 65.5 | 615 | 4 | US-08-840-713-35 Sequence 35, Appl1 |
| 22 | 823.5 | 65.5 | 617 | 4 | US-08-840-713-37 Sequence 37, Appl1 |
| 23 | 823.5 | 65.5 | 637 | 2 | US-08-235-838-14 Sequence 14, Appl1 |
| 24 | 823.5 | 65.5 | 637 | 2 | US-08-465-473B-14 Sequence 14, Appl1 |
| 25 | 823.5 | 65.5 | 711 | 1 | US-08-235-838-7 Sequence 7, Appl1 |
| 26 | 823.5 | 65.5 | 711 | 2 | US-08-465-473B-7 Sequence 7, Appl1 |
| 27 | 818.5 | 65.1 | 241 | 1 | US-08-235-838-5 Sequence 5, Appl1 |

| | | | | | |
|----|-------|------|-----|---|--------------------------------------|
| 28 | 818.5 | 65.1 | 241 | 2 | US-08-465-473B-5 Sequence 5, Appl1 |
| 29 | 816 | 64.9 | 259 | 4 | US-09-419-788-115 Sequence 115, App |
| 30 | 804 | 63.9 | 267 | 3 | US-09-485-737B-2 Sequence 2, Appl1 |
| 31 | 804 | 63.9 | 267 | 4 | US-10-071-485-2 Sequence 85, Appl1 |
| 32 | 804 | 63.9 | 541 | 3 | US-09-485-737B-95 Sequence 85, Appl1 |
| 33 | 804 | 63.9 | 541 | 4 | US-10-071-485-85 Sequence 90, Appl1 |
| 34 | 804 | 63.9 | 711 | 3 | US-09-485-737B-90 Sequence 90, Appl1 |
| 35 | 804 | 63.9 | 711 | 4 | US-10-071-485-90 Sequence 90, Appl1 |
| 36 | 803 | 63.8 | 284 | 3 | US-09-184-688-40 Sequence 40, Appl1 |
| 37 | 803 | 63.8 | 284 | 4 | US-09-504-262D-40 Sequence 40, Appl1 |
| 38 | 799.5 | 63.6 | 365 | 3 | US-08-875-811-53 Sequence 53, Appl1 |
| 39 | 799.5 | 63.6 | 366 | 3 | US-08-875-811-55 Sequence 55, Appl1 |
| 40 | 791.5 | 62.9 | 240 | 3 | US-09-485-737B-91 Sequence 91, Appl1 |
| 41 | 791.5 | 62.9 | 240 | 4 | US-10-071-485-91 Sequence 91, Appl1 |
| 42 | 782.5 | 62.2 | 287 | 4 | US-09-318-786-37 Sequence 37, Appl1 |
| 43 | 779 | 61.9 | 235 | 3 | US-09-485-737B-93 Sequence 93, Appl1 |
| 44 | 779 | 61.9 | 235 | 4 | US-10-071-485-93 Sequence 93, Appl1 |
| 45 | 766.5 | 60.9 | 230 | 3 | US-09-485-737B-102 Sequence 102, App |

ALIGNMENTS

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RESULT 1
US-08-133-804-6
Sequence 6, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teestra, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-6
Query Match 100.0%; Score 1258; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIQLVQSGPELKKPGETVKISCKASGYTFPANYGMNMKQAPGKGLKMMGMINTYTGQSTY 60
Db 1 EIQLVQSGPELKKPGETVKISCKASGYTFPANYGMNMKQAPGKGLKMMGMINTYTGQSTY 60
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| | | | |
|----|-----|---|-----|
| QY | 61 | ADDFKRRPFAFSLSTSTATHLQINNLRNDSATYTCARFEPAAWGGOTLVASASISS | 120 |
| Db | 61 | ADDFKRRPFAFSLSTSTATHLQINNLRNDSATYTCARFEPAAWGGOTLVASASISS | 120 |
| QY | 121 | SGSSSSSGSSSGSDIQMTQSPSSLASLGERVSLTCRASQDIGNSLTWLQGPDTIKRL | 180 |
| Db | 121 | SGSSSSSGSSSGSDIQMTQSPSSLASLGERVSLTCRASQDIGNSLTWLQGPDTIKRL | 180 |
| QY | 181 | IYATSSLDGVPKPRFSGSRSGSDYSLTSSLESEFPVYVYLCLOVAIPFYTGGGTNIETK | 240 |
| Db | 181 | IYATSSLDGVPKPRFSGSRSGSDYSLTSSLESEFPVYVYLCLOVAIPFYTGGGTNIETK | 240 |
| QY | 241 | RAD | 243 |
| Db | 241 | RAD | 243 |

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US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-6

Query Match 100.0%; Score 1258; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKPGETVYKISCKASGYTPANGNMWQAPKGGIKKMGWINTTYGOSTY 60
Db 1 EIQLVQSGPELKKPGETVYKISCKASGYTPANGNMWQAPKGGIKKMGWINTTYGOSTY 60
OY 61 ADDRKRERAFSLRTSATTAHAIQINNLRNEDSATYCARFGAYWGOGTLVSVSASISS 120
Db 61 ADDRKRERAFSLRTSATTAHAIQINNLRNEDSATYCARFGAYWGOGTLVSVSASISS 120

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| | | | |
|----|-----|---|-----|
| QY | 121 | SGSSSSSSSSSGSDTOMTQSPSSLSASIGERYVSLTCRASODIGNSLWMLQOEPDGTIKRL | 180 |
| | 121 | SGSSSSSSSSSSSDIOMTQSPSSLSASIGERYSLTCRASODIGNSLWMLQOEPDGTIKRL | 180 |
| Db | 121 | SGSSSSSSSSSSSDIOMTQSPSSLSASIGERYSLTCRASODIGNSLWMLQOEPDGTIKRL | 180 |
| QY | 181 | IYATSLDSDGVPRFSGSRGSDYSLTSSLESEDFFVYYCLQYAIFFYTFGGGTNLEIK | 240 |
| Db | 181 | IYATSLDSDGVPRFSGSRGSDYSLTSSLESEDFFVYYCLQYAIFFYTFGGGTNLEIK | 240 |
| QY | 241 | RAD 243 | |
| | 241 | | |
| Db | 241 | RAD 243 | |

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RESULT 3
US-08-461-386-6
; Sequence 6, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: Testa, Hurwitz & Thibault/Patent Department
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent'n Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-386-6

Query Match      100.0%; Score 1258; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.9e-105;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIQIVSGSPETIKKPGFETVYKISCKASGYTPFANYGNMNMKQAPGKGIKMGWINTYTGOSTY 60
DB      1 EIQIVSGSPETIKKPGFETVYKISCKASGYTPFANYGNMNMKQAPGKGIKMGWINTYTGOSTY 60
QY      61 ADDRKEPAPSLFETSAATTAHIIQINNLNREDSATYFCARRPFPAYWGQGLVSVSASISS 120
DB      61 ADDRKEPAPSLFETSAATTAHIIQINNLNREDSATYFCARRPFPAYWGQGLVSVSASISS 120
QY      121 SGGSSSSGGSSSGSDSIQMTQSPSISASLIGERVSLTCRASDIDIGSLTWLQEPDGTIKRL 180
DB      121 SGGSSSSGGSSSGSDSIQMTQSPSISASLIGERVSLTCRASDIDIGSLTWLQEPDGTIKRL 180
QY      181 IVATSSLDGVPKRPFGSGRSGSDYSLTSSLESDFVVVYLCIQYAIFFYTTGGGGINLEIK 240

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Db 181 IYATSSLDGVPKRRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240
QY 241 RAD 243
Db 241 RAD 243

RESULT 4
US-08-356-786-4
/ Sequence 4, Application US/08356786
/ Patent No. 5877305
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
/ TITLE OF INVENTION: Marker
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/356,786
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/831,967
/ FILING DATE: 06-FEB-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pitcher, Edmund R.
/ REGISTRATION NUMBER: 27,829
/ REFERENCE/DOCKET NUMBER: CRP-053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 248-7000
/ TELEFAX: (617) 248-7100
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 243 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-356-786-4

Query Match 100.0%; Score 1258; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 3.9e-105; Mismatches 0; Indels 0; Gaps 0;

Db 1 EIQLVQSGPELKKPGETYKISCKASGYTFANYGMMNMKQAPGKGLKMMGINTYTGOSTY 60
QY 1 EIQLVQSGPELKKPGETYKISCKASGYTFANYGMMNMKQAPGKGLKMMGINTYTGOSTY 60
Db 1 EIQLVQSGPELKKPGETYKISCKASGYTFANYGMMNMKQAPGKGLKMMGINTYTGOSTY 60
QY 61 ADDFERAFSLFETATTAHLQINNLRNEDSATYFCARFGFAYVGGGTLVSVASISSS 120
Db 61 ADDFERAFSLFETATTAHLQINNLRNEDSATYFCARFGFAYVGGGTLVSVASISSS 120
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
Db 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
Db 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
QY 181 IYATSSLDGVPKRRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240
Db 181 IYATSSLDGVPKRRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLEIK 240

QY 241 RAD 243
Db 241 RAD 243

RESULT 5
US-08-356-786-10
/ Sequence 10, Application US/08356786
/ Patent No. 5877305
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
/ APPLICANT: Oppermann, Hermann
/ APPLICANT: Houston, L. L.
/ APPLICANT: Ring, David B.
/ TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
/ TITLE OF INVENTION: Marker
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
/ STREET: Exchange Place, 53 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/356,786
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/831,967
/ FILING DATE: 06-FEB-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pitcher, Edmund R.
/ REGISTRATION NUMBER: 27,829
/ REFERENCE/DOCKET NUMBER: CRP-053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 248-7000
/ TELEFAX: (617) 248-7100
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 534 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-356-786-10

Query Match 96.5%; Score 1214; DB 2; Length 534;

Best Local Similarity 95.9%; Pred. No. 1e-100; Mismatches 8; Indels 2; Gaps 1;

QY 1 EIQLVQSGPELKKPGETYKISCKASGYTFANYGMMNMKQAPGKGLKMMGINTYTGOSTY 60
Db 290 EIQLVQSGPELKKPGETYKISCKASGYTFANYGMMNMKQAPGKGLKMMGINTYTGOSTY 349
QY 61 ADDFERAFSLFETATTAHLQINNLRNEDSATYFCARFGFAYVGGGTLVSVASISSS 120
Db 350 ADDFERAFSLFETATTAHLQINNLRNEDSATYFCARFGFAYVGGGTLVSVASISSS 409
QY 121 --SGSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIK 178
Db 410 GCGSGCGGSGGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIK 469
QY 179 RLIVATSSLDGVPKRRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLE 238
Db 470 RLIVATSSLDGVPKRRFSGSRSSGSDYSLTISLSESDPVVYVCLOYAFPTTGGGNTLE 529
QY 239 IKRAD 243

Db 530 IKRAD 534

RESULT 6

US-08-133-804-2

Sequence 2, Application US/08133804

Patent No. 5534254

GENERAL INFORMATION:

APPLICANT: Husecon, James S.

APPLICANT: Oppermann, Hermann

APPLICANT: Houston, L. L.

APPLICANT: Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins For

TITLE OF INVENTION: Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-133-804-2

Query Match 72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 60
Db 3 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 62
QY 61 ADDPKERAFSELETSATTAHLQINNLKNEDESATYFCARRF---GFAVWGQGTIVSVAS 116
Db 63 AEEFKRFAFSELETSATTAHLQINNLKNEDESATYFCARRF---GFAVWGQGTIVSVAS 121
QY 117 ISSSSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOQEPDGT 176
Db 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFMSTSVGDRVSIKCAQSDVSTAVAWYQKPGQS 178
QY 177 IKRLIYATSLDGGVPRKFRSGSGSDYSLTSSLESEDFVYVYCLQYAIFFYTGQGTN 236
Db 179 PKLLIYMTSTHTGVPRFTSSGSGDTYTLTSSVQAEALALHYCQGHYRVYTFGGGK 238
QY 237 LEIKRAD 243
Db 239 LEIKRAD 245

RESULT 7

US-08-461-184-8

Sequence 8, Application US/08461184

Patent No. 5631158

GENERAL INFORMATION:

APPLICANT: DORAI, HAIMANTI

APPLICANT: OPPERMAN, HERMANN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN

TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01718

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,184

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/143,498

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: KELLEY, ROBIN D

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: CRP093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7000

TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-184-8

Query Match 72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 60
Db 3 EIQLVSGPELKKRGRTYKISCKASGYTFANYGMNMKQAPGKGLKMMGWINTYTGQSTY 62
QY 61 ADDPKERAFSELETSATTAHLQINNLKNEDESATYFCARRF---GFAVWGQGTIVSVAS 116
Db 63 AEEFKRFAFSELETSATTAHLQINNLKNEDESATYFCARRF---GFAVWGQGTIVSVAS 121
QY 117 ISSSSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOQEPDGT 176
Db 122 -SSSSSSSSSSSSSS--SDIWMTQSPKFMSTSVGDRVSIKCAQSDVSTAVAWYQKPGQS 178
QY 177 IKRLIYATSLDGGVPRKFRSGSGSDYSLTSSLESEDFVYVYCLQYAIFFYTGQGTN 236
Db 179 PKLLIYMTSTHTGVPRFTSSGSGDTYTLTSSVQAEALALHYCQGHYRVYTFGGGK 238
QY 237 LEIKRAD 243
Db 239 LEIKRAD 245

RESULT 8

US-08-463-675-8

Sequence 8, Application US/08463675

Patent No. 5658763

GENERAL INFORMATION:

```

; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,675
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-463-675-8

```

```

Query Match      72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY      1 EIQLVQSGBELKKPGETYKISCKASGYTFPANYGMNMKQAPGKGLKMGWINTTNGQSTY 60
DB      3 EIQLVQSGBELKKPGETYKISCKASGYTFPANYGMNMKQAPGKGLKMGWINTTNGEPY 62
QY      61 ADFKRFAPFSLTETATTAHLQINLNKEDSATYFCARF---GPAVYGQGLTVSVAS 116
DB      63 AEFKGRAPFSLTETASTAYLQINLNKEDTATYFCGRQFITYGGFANMGQGLTVVSA- 121
QY      117 ISSSSGSSSSGSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEPDGT 176
DB      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDRVSIKCKASQDVSTAVANYQOKPGQS 178
QY      177 IKRLIYATSSLDGVPKRFSGRSQSDYSLTISLSEDFVYVYICLQVAFIPYTFGGGTN 236
DB      179 PRLIYMTSTRHTGVDPFTGSGGTDYTLTITSSVOAEDLALHYCOQHRYRVEYTFGGGTK 238
QY      237 LEIKRAD 243
DB      239 LEIKRAD 245

```

```

RESULT 9
US-08-464-589-8
; Sequence 8, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA

```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-589-8

```

```

Query Match      72.7%; Score 914; DB 1; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-74;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```

```

QY      1 EIQLVQSGBELKKPGETYKISCKASGYTFPANYGMNMKQAPGKGLKMGWINTTNGQSTY 60
DB      3 EIQLVQSGBELKKPGETYKISCKASGYTFPANYGMNMKQAPGKGLKMGWINTTNGEPY 62
QY      61 ADFKRFAPFSLTETATTAHLQINLNKEDSATYFCARF---GPAVYGQGLTVSVAS 116
DB      63 AEFKGRAPFSLTETASTAYLQINLNKEDTATYFCGRQFITYGGFANMGQGLTVVSA- 121
QY      117 ISSSSGSSSSGSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEPDGT 176
DB      122 -SSSSGSSSSGSSS--SDIWMQSPKFMSTSVGDRVSIKCKASQDVSTAVANYQOKPGQS 178
QY      177 IKRLIYATSSLDGVPKRFSGRSQSDYSLTISLSEDFVYVYICLQVAFIPYTFGGGTN 236
DB      179 PRLIYMTSTRHTGVDPFTGSGGTDYTLTITSSVOAEDLALHYCOQHRYRVEYTFGGGTK 238
QY      237 LEIKRAD 243
DB      239 LEIKRAD 245

```

```

RESULT 10
US-08-461-838-2
; Sequence 2, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Opperman, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-461-838-2

```

Query Match 72.7%; Score 914; DB 1; Length 250;

Best Local Similarity 71.7%; Pred. No. 3,1e-74; Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

```

QY 1 EIQLVSGPELKKPGETVTKISCKASGYTFANYGMNMWKOAPGKGLKMGMINITYGQSTY 60
DB 3 EIQLVSGPELKKPGETVTKISCKASGYTFANYGMNMWKOAPGKGLKMGMININTGEPT 62
QY 61 ADDFKRPAFSLTSTATTALQINLRNDSATYFCARF---GPAWGGCTLVSVAS 116
DB 63 AEEFKRPAFSLTSTATTALQINLRNDSATYFCARF---GPAWGGCTLVSVAS 121
QY 117 ISSSSSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOOEPGT 176
DB 122 -SSSSSSSSSSSS--SDIWMTQSPKFMSTVGDVSVISCKASQDVSTAVMYQKPGQS 178
QY 177 IKRLIVATSLDGVGPKRFGSGRSQSDYSLTISLSEDFVYYCLQVAFPTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDFRTGSGSGTDYTLTISVQADLALHYCQHRYRVPTFGGGTK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

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RESULT 11
US-08-461-386-2

```

; Sequence 2, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

```

```

; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-461-386-2

```

Query Match 72.7%; Score 914; DB 2; Length 250;

Best Local Similarity 71.7%; Pred. No. 3,1e-74; Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

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QY 1 EIQLVSGPELKKPGETVTKISCKASGYTFANYGMNMWKOAPGKGLKMGMINITYGQSTY 60
DB 3 EIQLVSGPELKKPGETVTKISCKASGYTFANYGMNMWKOAPGKGLKMGMININTGEPT 62
QY 61 ADDFKRPAFSLTSTATTALQINLRNDSATYFCARF---GPAWGGCTLVSVAS 116
DB 63 AEEFKRPAFSLTSTATTALQINLRNDSATYFCARF---GPAWGGCTLVSVAS 121
QY 117 ISSSSSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTWLOOEPGT 176
DB 122 -SSSSSSSSSSSS--SDIWMTQSPKFMSTVGDVSVISCKASQDVSTAVMYQKPGQS 178
QY 177 IKRLIVATSLDGVGPKRFGSGRSQSDYSLTISLSEDFVYYCLQVAFPTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDFRTGSGSGTDYTLTISVQADLALHYCQHRYRVPTFGGGTK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

```

RESULT 12
US-08-356-786-16

```

; Sequence 16, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fletcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-16

Query Match 70.8%; Score 891; DB 2; Length 622;
Best Local Similarity 70.4%; Pred. No. 1,2e-71;
Matches 174; Conservative 32; Mismatches 33; Indels 8; Gaps 3;

QY 1 EIQLVSGELKPKGETVYKISCKASGYTFYNTGMMMKQAPGKGLKMGWINTYTGQSTY 60
DB 3 EIQLVSGELKPKGETVYKISCKASGYTFYNTGMMMKQAPGKGLKMGWINTYTGQSTY 62
QY 61 ADDFERFAPSLETATTAHLQINNLRNEDSATYFCARF---GPAVMGQGLTVSVAS 116
DB 63 AAEFGKRFPSLETSTAYVLIQINLNKEDTAYFCGRQFTYGGFANMGQGLTVVSA- 121
QY 117 ISSSSSSSSSSSSSSGSDIQMTQSPSSLSASIGERYSLICRASQDIGNSLTWLQOEPRDT 176
DB 122 -SSSSSSSSSSSS--SDIVMTQSPKFMSTVGDNRVSIKCKASQDVSTAVANYQOKPQGS 178
QY 177 IKRLIYATSSLDGVPKRFSGSGSDYSLTISLESDFVYVYICLOYALFPYTFGGGTNL 236
DB 179 PKLLIYVTRHTRGVDPFTGSGSGTDYTLTISVQADLALHYCQOHYRVAYTFGRGTX 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

RESULT 13
US-08-488-113B-148
Sequence 148, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-148

Query Match 65.7%; Score 827; DB 1; Length 240;
Best Local Similarity 65.8%; Pred. No. 1.9e-66;
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 EIQLVSGELKPKGETVYKISCKASGYTFYNTGMMMKQAPGKGLKMGWINTYTGQSTY 60
DB 1 EIQLVSGGGLVKGGSVYRISCAASGYTFYNTGMMVVRQAPGKGLKMGWINTYTGQSTY 60
QY 61 ADDFERFAPSLETATTAHLQINNLRNEDSATYFCARF---FGPAVMGQGLTVSVAS 117
DB 61 ADSFKGRFPSLDBDKNTRAYLIQINLRAEDTAYCTRGYMYRFDVWQGTIVYS--- 117
QY 118 SSSSSSSSSSSSSGSDIQMTQSPSSLSASIGERYSLICRASQDIGNSLTWLQOEPRDT 177
DB 118 SGGGSGGGGSGGSGSDIQMTQSPSSLSASVGDVYITICRASQDINSYLSWFOQKPKAP 177
QY 178 KRLIYATSSLDGVPKRFSGSGSDYSLTISLESDFVYVYICLOYALFPYTFGGGTNL 237
DB 178 KTLIYANRLBSGVPKRFSGSGSDYSLTISLQYEDRGIYCOQYDPSFWTFGGGTNL 237
QY 238 EIK 240
DB 238 EIK 240

RESULT 14
US-08-477-484B-148
Sequence 148, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago

```
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-148

Query Match      65.7%; Score 827; DB 1; Length 240;
Best Local Similarity 65.8%; Pred. No. 1.9e-66;
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 EIQLVSGGELKKPGEIVKISCKASGYTFANYGMNMWQAQPKGLKMGWINTYTGOSTY 60
DB 1 EIQLVSGGGLVYRPGSVIRISCAASGYTTNVMNVRAQPKGLKMGWINTHGEPTY 60
QY 61 ADDPKERFAPSLETATTAHLQINLRNEDSATYFCARR---FGPAYWGQGLTVSVASAI 117
DB 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRGYDVPFWWGQGLTVTVS--- 117
QY 118 SSSSGSSSSSSSSSGSDIQMTQSPSSLASLGERVSLTCRASQDIGNSLTWLQOEPPDGTI 177
DB 118 SGGGGSGGGSGGGSDIQMTQSPSSLASVGDVITTCRASQDINSYLSWFOQKPKAP 177
QY 178 KRLIYATSSLDSGVPRPFRSGRSGSDYSLTISLSSEDPVYVYCCQYALFPTTGGGNTL 237
DB 178 KTLIYRANLLESGVPRPFRSGSGSDYTLTISLQYEDFGIYCCQGYDSSPWTFGGNTL 237
QY 238 EIK 240
DB 238 EMK 240

RESULT 15
US-08-646-360-148
; Sequence 148, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
```

```
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-148

Query Match      65.7%; Score 827; DB 2; Length 240;
Best Local Similarity 65.8%; Pred. No. 1.9e-66;
Matches 160; Conservative 28; Mismatches 49; Indels 6; Gaps 2;

QY 1 EIQLVSGGELKKPGEIVKISCKASGYTFANYGMNMWQAQPKGLKMGWINTYTGOSTY 60
DB 1 EIQLVSGGGLVYRPGSVIRISCAASGYTTNVMNVRAQPKGLKMGWINTHGEPTY 60
QY 61 ADDPKERFAPSLETATTAHLQINLRNEDSATYFCARR---FGPAYWGQGLTVSVASAI 117
DB 61 ADSFKGRFTFSLDSSKNTAYLQINSLRAEDTAVYFCTRRGYDVPFWWGQGLTVTVS--- 117
QY 118 SSSSGSSSSSSSGSDIQMTQSPSSLASLGERVSLTCRASQDIGNSLTWLQOEPPDGTI 177
DB 118 SGGGGSGGGSGGGSDIQMTQSPSSLASVGDVITTCRASQDINSYLSWFOQKPKAP 177
QY 178 KRLIYATSSLDSGVPRPFRSGRSGSDYSLTISLSSEDPVYVYCCQYALFPTTGGGNTL 237
DB 178 KTLIYRANLLESGVPRPFRSGSGSDYTLTISLQYEDFGIYCCQGYDSSPWTFGGNTL 237
QY 238 EIK 240
DB 238 EMK 240
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| | | | |
|----|-----|-----|-----|
| Oy | 238 | BIK | 240 |
| | | : | |
| Db | 238 | EMK | 240 |

Search completed: April 4, 2005, 16:00:49
Job time : 129.217 secs

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CC present sequence represents a VL domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 53; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
DB 24 RASQDIGNSLT 34

RESULT 2
AAW02280
ID AAW02280 standard; protein; 243 AA.

AC AAW02280;

DT 25-MAR-2003 (revised)
DT 29-OCT-1996 (first entry)

DE 520C9 anti-c-erbB-2 two single chain Fv construct.

KW 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;
KW construct; polypeptide linker; C-terminal amino acid sequence;
KW in vivo imaging; drug targeting experiment; homodimer; increased;
KW binding avidity; tissue retention time.

OS Homo sapiens.

PH Key Location/Qualifiers
FT Peptide 118..133
FT /label= linker

PN US5534254-A.

PD 09-JUL-1996.

PF 07-OCT-1993; 93US-00133804.

PR 06-FEB-1992; 92US-00831967.

XX (CHIR) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1996-333194/33.

DR N-PSDB; AAT36880.

PT Compens. contg. antigen-targeting antibody fragment constructs -
PT comprising dimer of single-chain Fv fragments.

PS Example 1; Col 33-36; 30pp; English.

XX Variable heavy (VH) and variable light (VL) genes were cloned from a
CC 520C9 hybridoma cDNA library, using probes directed toward the antibody
CC constant and joining regions. A two single chain Fv (sfv) gene was
CC constructed by connecting the VH and VL genes with a Ser rich polypeptide
CC linker. The resulting 520C9 two sfv gene, which encodes the present
CC sequence, was inserted into an expression vector, transformed into E.
CC coli, and protein expression induced by the addn. of IPTG to the culture
CC medium. A compen. comprising a carrier and the 2 sfv protein prod. can be
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv
CC protein prod. is a homodimer, in which both fragments target the same
CC antigen, therefore giving greater binding avidity and longer tissue
CC retention times, compared to individual sfv protein prod. fragments.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 243 AA;

Query Match 100.0%; Score 53; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
DB 157 RASQDIGNSLT 167

RESULT 3
AAW53170
ID AAW53170 standard; protein; 243 AA.

AC AAW53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;
KW tumour; diagnosis; ss.

OS Synthetic.

OS Mus sp.

PN US5753204-A.

PD 19-MAY-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR) CHIRON CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1998-311318/27.

DR N-PSDB; AAV21798.

PT Imaging of antigens in vivo - using dimers of single-chain antibody Fv
PT fragments.

PS Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)
CC construct. This was constructed by connecting the Vh and Vl genes with a
CC DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can
CC be used in the methods of invention of imaging a preselected antigen
CC expressed in a mammal. The methods are used in magnetic resonance imaging
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
CC constructs have enhanced properties as in vivo targeting agents in
CC comparison with intact monoclonal antibodies or their Fab fragments. The
CC dimeric constructs permit the in vivo targeting of an epitope on an
CC antigen with greater apparent avidity, including greater tumour
CC specificity, tumour localisation and tumour retention properties than
CC that of the Fab fragment having the same CDRs as the construct
XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 53; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
DB 157 RASQDIGNSLT 167

RESULT 4

```

AAW80424
ID AAW80424 standard; protein; 243 AA.
XX
AC AAW80424;
XX
DT 28-JAN-1999 (first entry)
XX
DE 520C9 gFv sequence.
XX
XX 520C9 gFv; antigen; tumour cell; antibody 520C9; targeted delivery;
KM antigen-expressing cell.
XX
OS Synthetic.
XX
PN US5837846-A.
XX
PD 17-NOV-1998.
XX
PF 05-JUN-1995; 95US-00461386.
XX
PR 06-FEB-1992; 92US-00831967.
XX
PR 07-OCT-1993; 93US-00133804.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Oppermann H, Houston LL, Huston JS, Ring DB;
XX
DR WPI; 1999-023541/02.
XX
DR N-PSDB; AAV63399.
XX
PT Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.
XX
PS Example 1; Col 35-36; 29pp; English.
XX
XX The present sequence represents an antibody 520C9 gFv. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs
CC or 99m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumours (especially of ovary or breast)
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 53; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
DB 157 RASQDIGNSLT 167

RESULT 5
ABW00716
ID ABW00716 standard; protein; 243 AA.
XX
AC ABW00716;
XX
DT 15-JAN-2004 (first entry)
XX
DE 520C9 gFv protein.
XX
XX Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
KM gFv.
XX
OS Unidentified.
XX
PN US2002168375-A1.

```

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XX
PD 14-NOV-2002.
XX
PF 21-JUN-2001; 2001US-00887853.
XX
XX 06-FEB-1992; 92US-00831967.
XX
PR 07-OCT-1993; 93US-00133804.
XX
PR 05-JUN-1995; 95US-00462641.
XX
PR 26-APR-2000; 2000US-00558741.
XX
PA (CHIR ) CHIRON CORP.
XX
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
DR WPI; 2003-765156/72.
XX
DR N-PSDB; AAD61485.
XX
XX
PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
PS Example 1; Page 19-20; 30pp; English.
XX
XX The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibits cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 gFv protein. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 53; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSLT 11
DB 157 RASQDIGNSLT 167

RESULT 6
AAR39569
ID AAR39569 standard; protein; 246 AA.
XX
AC AAR39569;
XX
DT 25-MAR-2003 (revised)
XX
DT 07-FEB-1994 (first entry)
XX
DE Sequence of 520C9 gFv protein.
XX
XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KM biosynthetic single polypeptide chain binding site; sb.
XX
OS Synthetic.
XX
PN WO9316185-A2.
XX
PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
XX
PR 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
PA (CETU ) CETUS ONCOLOGY CORP.
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX

```

DR WPI: 1993-272889/34.
 DR N-PSDB; AAQ46084.
 XX
 FT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
 PT imaging or treating breast or ovarian cancer etc.
 XX
 PS Claim 4; Page 60-61, 87pp; English.
 XX
 CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour
 CC cells, such as breast and ovarian tumour cells, which is an approx.
 CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
 CC 5.3 (see AAQ46083, AAR39568). A single chain Fv (scFv) is a covalently
 CC linked VH-VL heterodimer which is expressed from a gene fusion including
 CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such
 CC linker sequences are set forth in AA residues 116-135 in AAR39569, which
 CC includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084
 CC for the 520C9 monoclonal antibody, a single chain polypeptide can be
 CC produced having a binding affinity for a C-erbB-2 related antigen. 'X' in
 CC AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 246 AA;
 SQ
 Query Match 100.0%; Score 53; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASODIGNSLT 11
 Db 157 RASODIGNSLT 167
 RESULT 7
 AAU04944
 ID AAU04944 standard; protein; 267 AA.
 AC AAU04944;
 XX
 DT 06-AUG-2003 (revised)
 DT 24-OCT-2001 (first entry)
 XX
 DE Humanised anti-p185 single chain antibody; 520C9H.
 XX
 KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
 KW cancer; tumour; adenocarcinoma.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Location/Qualifiers
 FT 53..57
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 72..88
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 121..126
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 138..152
 FT /label= Synthetic peptide linker
 FT /note= "Links the heavy chain to the light chain"
 FT 176..186
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 202..208
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 241..249
 FT /label= CDR
 FT /note= "Complementarity determining region"

FT Region 260..267
 FT /label= Glu_Glu epitope
 XX
 XX
 PN WO200153354-A2.
 XX
 XX
 PD 26-UTL-2001.
 XX
 XX
 PF 19-JAN-2001; 2001WO-US001919.
 XX
 PR 20-JAN-2000; 2000US-0177258P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
 PA (HAMI-) HAMILTON REGIONAL CANCER CENT.
 XX
 PI Austin R, Kwok CS, Ring DB;
 XX
 DR WPI: 2001-451904/48.
 DR N-PSDB; AAS09507.
 XX
 PT Novel immunoconjugate useful for inhibiting tumor cell growth in vivo
 PT comprises a humanized anti-p185 antibody linked to an interleukin-2
 PT polypeptide.
 PS
 PS Claim 7; Fig 9; 74pp; English.
 XX
 CC The sequence represents a humanised anti-p185 single chain antibody which
 CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion
 CC protein. The fusion protein (or immunoconjugate) is used to inhibit the
 CC growth of tumours or cancers particularly those characterised by
 CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
 CC benign tumours of the breast, renal system, salivary gland, and
 CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
 CC correct OS field.)
 CC
 SQ Sequence 267 AA;
 SQ
 Query Match 100.0%; Score 53; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASODIGNSLT 11
 Db 176 RASODIGNSLT 186
 RESULT 8
 AAU04945
 ID AAU04945 standard; protein; 409 AA.
 AC AAU04945;
 XX
 XX
 DT 06-AUG-2003 (revised)
 DT 24-OCT-2001 (first entry)
 XX
 DE Humanised anti-p185 antibody/IL-2 fusion protein.
 XX
 KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
 KW cancer; tumour; adenocarcinoma; fusion protein.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Location/Qualifiers
 FT 1..22
 FT /label= Signal peptide
 FT 23..409
 FT /label= Mature fusion protein
 FT 23..259
 FT /label= Humanised_antibody_520C9H
 FT 53..57
 FT Region

```

FT /label= CDR
FT /note= "Complementarity determining region"
FT Region
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region
FT /label= CDR
FT /note= "Complementarity determining region"
FT Misc-difference
FT /note= "Encoded by GGG"
FT Peptide
FT /label= Synthetic peptide linker
FT /note= "Links the heavy chain to the light chain"
FT Region
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region
FT /label= CDR
FT /note= "Complementarity determining region"
FT Region
FT /label= CDR
FT /note= "Complementarity determining region"
FT Peptide
FT /label= Synthetic linker peptide
FT /note= "Links the antibody to the IL-2 molecule"
FT Protein
FT /label= IL_2
FT Misc-difference
FT /note= "Encode by ACA"
FT WO20015354-A2.
FT 26-JUL-2001.
FT 19-JAN-2001; 2001WO-US001919.
FT 20-JAN-2000; 2000US-0177258P.
FT (CHIR ) CHIRON CORP.
FT (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
FT (HAMI-) HAMILTON REGIONAL CANCER CENT.
FT Austin R, Kwok CS, Ring DB;
FT WPI; 2001-451904/48.
FT N-PSDB; AAS09508.
FT Novel immunconjugate useful for inhibiting tumor cell growth in vivo
FT comprises a humanized anti-p185 antibody linked to an Interleukin-2
FT polypeptide.
FT Claim 13; Fig 11; 74pp; English.
XX The sequence represents a humanised anti-p185 (520C9) single chain
XX antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein
XX (or immunconjugate) is used to inhibit the growth of tumours or cancers
XX particularly those characterised by overexpression of p185 e.g. human
XX adenocarcinomas and malignant and/or benign tumours of the breast, renal
XX system, salivary gland, gastrointestinal tract or gastric tumours.
XX (Updated on 06-AUG-2003 to correct OS field.)
SQ Sequence 409 AA;
Query Match 100.0%; Score 53; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASODIGNSLT 11
DB 176 RASODIGNSLT 186
RESULT 9

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AAR39571
ID AAR39571 standard; protein; 534 AA.
XX AAR39571;
AC AAR39571;
XX 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX Sequence of G-FIT.
DE Tumour antigen; c-erbB-2; G-FIT.
XX Tumour antigen; c-erbB-2; G-FIT.
XX Synthetic.
XX WO9316185-A2.
XX 19-AUG-1993.
XX 05-FEB-1993; 93WO-US001055.
XX 06-FEB-1992; 92US-00831967.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX (CERTU ) CERTUS ONCOLOGY CORP.
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX WPI; 1993-272889/34.
XX N-PSDB; AAQ46086.
XX New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
XX imaging or treating breast or ovarian cancer etc.
XX Example; Page 65-68; 87pp; English.
XX c-erbB-2 refers to a protein antigen expressed on the surface of tumour
XX cells, such as breast and ovarian tumour cells, which is an approx.
XX 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
XX 5.3 (see AAQ46083, AAR39568). (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 534 AA;
Query Match 100.0%; Score 53; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASODIGNSLT 11
DB 448 RASODIGNSLT 458
RESULT 10
AAY06388
ID AAY06388 standard; protein; 109 AA.
XX AAY06388;
AC AAY06388;
XX 06-SEP-1999 (first entry)
DT Humanised LM609 antibody VL domain.
XX Humanised LM609 antibody VL domain.
XX Humanised antibody; antibody humanisation; antibody engineering; LM609;
XX monoclonal antibody; complementarity determining region; CDR grafting;
XX mouse; human; integrin; apoptosis; angiogenesis; cancer; therapy;
XX diagnosis.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..2
XX /note= "vector-encoded residues"
FT

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FT Region 24. .34
FT /note= "CDR1"
FT Region 50. .56
FT /note= "CDR2"
FT Region 89. .97
FT /note= "CDR3"
XX WO9929888-A1.
XX 17-JUN-1999.
PD
XX 04-DEC-1998; 98WO-US025828.
XX
XX 05-DEC-1997; 97US-00986016.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies.
XX
XX Disclosure; Page 52; 55pp; English.
XX
XX This sequence represents the light chain variable region of a humanised
XX LM609 antibody. LM609 is directed to human integrin alpha-v beta-3. It
XX selectively promotes apoptosis of vascular cells that have been
XX stimulated to undergo angiogenesis, making it a tool for cancer diagnosis
XX and therapy. The invention provides humanised antibodies, especially
XX humanised LM609. In such humanized antibodies, a light chain CDR from a
XX mouse antibody such as LM609 is grafted onto a human light chain, and a
XX heavy chain CDR from a mouse antibody is grafted onto a human antibody
XX having the desired specificity is selected. By preserving the original
XX CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see
XX AA05371-72), the humanisation strategy ensures epitope conservation
XX
XX Sequence 109 AA;
SQ
Query Match 90.6%; Score 48; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQDIGNSL 10
DB 24 RASQDIGNSL 33
RESULT 11
AAM50879
ID AAM50879 standard; protein; 112 AA.
XX
XX AAM50879;
AC
XX
XX 07-MAY-2002 (first entry)
DT
XX
XX Anti-bovine prion protein peptide antibody light chain.
XX
XX Prion; prion protein; PrP; PrPC; PrPSc; antibody; Fab; mouse; ungulate;
XX infection; bovine spongiform encephalopathy; BSE; diagnosis; therapy.
XX
XX Mus musculus.
XX
XX WO200210335-A2.
XX
XX 07-FEB-2002.
XX
XX 17-JUL-2001; 2001WO-US022648.
XX
XX 27-JUL-2000; 2000US-00627218.
XX
XX (REGC ) UNIV CALIFORNIA.

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PA (SCRI ) SCRIPPS RES INST.
XX
XX Prusiner SB, Safar J, Williamson AR, Burton DR;
XX WPI; 2002-195957/25.
XX
XX Novel antibody useful for detecting infectious prions, particularly
XX pathogenic scrapie isoform of the prion protein, PrPSc in an ungulate,
XX especially cow, binds to native ungulate prion protein C in situ.
XX
XX Example 1; Page 41; 63pp; English.
XX
XX The present sequence is that of the light chain of a recombinant Fab
XX antibody fragment (Clone P) that binds tightly to denatured bovine PrPSc
XX but not to the native conformation of the same protein in CD10 formatted
XX ELISA. The presence of PrPSc in tissues of humans or animals is
XX indicative of prion infection. The Fab was generated against the 96-105
XX region of bovine prion protein (PrP). Clone P binds to an epitope (see
XX AAM50886-87) that is present in all ungulate PrP sequences, including
XX bovine, and also in other species such as human, sheep and mouse. The P
XX recombinant antibody fragments (Fabs) were isolated from mouse CDNA and
XX cloned into a vector that expressed human-mouse chimeric Fabs in
XX Escherichia coli. The purified Fabs were labeled with Europium, giving an
XX Fab designated Eu-(HuM)Fab P. This is an example of antibodies of the
XX invention that specifically bind with a high degree of binding affinity
XX to a native ungulate PrPSc in situ and/or a denatured ungulate PrPSc, but
XX not to a native ungulate PrPC in situ. The antibodies may specifically
XX bind to epitopes of PrPC of a specific species of animal or to 1 or more
XX types of PrPC proteins from 1 or more species of ungulates. The
XX antibodies are useful for the detection of prion infection in ungulates,
XX particularly cattle. A fast, efficient, cost-effective assay is achieved.
XX The assay can be used to screen for the presence of PrPSc in products
XX such as pharmaceuticals (derived from natural sources), food, cosmetics
XX etc. The antibodies can be used with a compound that denatures PrPSc
XX thereby providing a means of differentiating levels of PrPC and
XX PrPC+PrPSc in a sample. The invention also provides a therapeutic
XX antibody which prevents or treats prion disease in ungulates, and
XX specifically in cattle, and a means for certifying certain products as
XX being prion free
XX
XX Sequence 112 AA;
SQ
Query Match 84.9%; Score 45; DB 5; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQDIGNSL 10
DB 24 RASQDIGNSL 33
RESULT 12
ADM78135
ID ADM78135 standard; peptide; 11 AA.
XX
XX ADM78135;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human SUB3-86 antibody variable light chain CDR1 peptide region.
XX
XX monoclonal antibody; adenylate kinase isozyme 3;
XX complementarity determining region; CDR; heart disease; marker AK3;
XX biochemical; human; variable; light chain.
XX
XX Homo sapiens.
XX
XX WO2004029094-A1.
XX
XX 08-APR-2004.
XX
XX 27-SEP-2003; 2003WO-KR001979.
XX

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PR 28-SEP-2002; 2002KR-00059211.
XX
PA (KIMH/) KIM H.
XX
PI Kim H;
XX
DR WPI; 2004-316088/29.
XX
PT New monoclonal antibody specific to human mitochondrial adenylate kinase
PT isozyme 3, useful for preparing a composition for detecting a heart
PT disease marker AK3.
XX
PS Claim 1; SEQ ID NO 98; 126pp; English.
XX
CC The invention relates to a novel monoclonal antibody specific to
CC adenylylate kinase isozyme 3, comprising 4 or more of 6 complementarily
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
CC invention further relates to: a composition comprising the monoclonal
CC antibody for detecting a heart disease marker AK3; a kit comprising the
CC monoclonal antibody for the diagnosis of heart disease; and a method of
CC detecting a heart disease marker AK3. The monoclonal antibody is useful
CC for preparing a composition for detecting a heart disease marker AK3. The
CC monoclonal antibody reduces false positive results of the conventional
CC biochemical markers. This sequence represents a human antibody variable
CC light chain CDR peptide region of the invention.
XX
SQ Sequence 11 AA;

Query Match 81.1%; Score 43; DB 8; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 1 RASQDIGSSL 10

RESULT 13
AAR80078
ID AAR80078 standard; protein; 90 AA.
XX
AC AAR80078;
XX
DT 22-MAY-1996 (first entry)
XX
DE Mouse derived light chain RT3 phage antibody pattern A.
XX
KW Light chain; RT3; murine; catalytic antibody; bacteriophage; pattern A.
XX
OS Mus musculus.
XX
XX
XX Location/Qualifiers
XX Key 1..15
XX Region /note= "framework region 1"
XX Region 16..26 /note= "complementarity determining region 1"
XX Region 27..40 /note= "complementarity determining region 2"
XX Region 41..47 /note= "framework region 2"
XX Region 48..78 /note= "complementarity determining region 2"
XX Region 79..88 /note= "framework region 3"
XX Region 89..90 /note= "complementarity determining region 3"
XX Region /note= "framework region 4 N-terminal fragment"
XX
XX WO9527045-A1.
XX
XX 12-OCT-1995.
XX
XX 30-MAR-1994; 94WO-US003420.
XX
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```
PR 30-MAR-1994; 94WO-US003420.
XX
PA (IGEN-) IGEN INC.
XX
PI Smith RG, Mc Cafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
PI Kenten JH, Martin MT, Tiltmae RC, Williams RO;
XX
XX WPI; 1995-358624/46.
XX
DR N-PSDB; AAT04625.
XX
PT Production of catalytic antibodies displayed on phage - by generating a
PT gene library of antibody-derived domains and expressing it in phage
PT vectors.
XX
XX
XX Disclosure; Fig 9; 133pp; English.
XX
XX AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
XX The DNA was used in the prepn. of catalytic antibody (CA) producing
XX bacteriophage. The CAs can be used to activate/deactivate a biological
XX function in an animal by enhancing the rate of cleavage, or formation of
XX a specific bond within a mol. in vivo
XX
SQ Sequence 90 AA;

Query Match 81.1%; Score 43; DB 2; Length 90;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 16 RASQDIGSSL 25

RESULT 14
AAW95480
ID AAW95480 standard; protein; 92 AA.
XX
AC AAW95480;
XX
DT 29-MAR-1999 (first entry)
XX
DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
XX
KW Catalytic; antibody; phage display; immunising; phage expression vector;
KW produg; scFV.
XX
XX
XX Mus sp.
XX
XX US5855885-A.
XX
XX 05-JAN-1999.
XX
XX 14-JUL-1994; 94US-00273146.
XX
XX 22-JAN-1993; 93US-00007684.
XX
XX (MCCA/) MCCAFFERTY J.
XX (CHIS/) CHISWELL D.
XX (DARS/) DARSLEY M J.
XX (TITM/) TITMAS R C.
XX (MART/) MARTIN M T.
XX (KENT/) KENTEN J H.
XX (SMIT/) SMITH R.
XX (FITZ/) FITZGERALD K.
XX (WILL/) WILLIAMS R O.
XX
XX Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
XX Kenten JH, Chiswell D, McCafferty J, Tiltmae RC;
XX
XX WPI; 1999-105036/09.
XX
XX N-PSDB; AAX00879.
XX
XX Production of catalytic antibodies displayed on bacteriophages -
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```

PR  comprises generating a gene library of antibody-derived domains inserting
PT  coding into a phage expression vector and isolating the catalytic
PR  antibodies.
XX
PS  Example 4; Fig 11; 117pp; English.
XX
CC  The invention relates to methods for producing catalytic antibodies
CC  displayed on a phage. The method comprises: (a) generating a gene library
CC  of antibody-derived domains; (b) inserting coding for the domains into a
CC  phage expression vector; and (c) isolating the catalytic antibodies. The
CC  phage expression vector incorporates a histidine peptide in tandem with a
CC  myc peptide. The catalytic antibodies can be isolated by preparing an
CC  antigen; optionally immunising an animal with the antigen; generating a
CC  library of VH and VL domains from the immunised animal; cloning the VH
CC  and VL domains into a phage expression vector to generate phage display
CC  antibodies; selecting phage display antibodies which bind specifically to
CC  the antigen; screening the selected phage display antibodies for
CC  catalytic activity to substrate; and isolating the catalytic antibodies,
CC  where the phage expression vector incorporates a histidine peptide in
CC  tandem with a myc peptide. The processes are used to produce catalytic
CC  antibodies, which can be used for in vivo activation of a prodrg. The
CC  present sequence represents a genetic sequence of light chain PCR pattern
CC  C from mouse derived RT3 phage antibodies
XX
SQ  Sequence 92 AA;
XX
Query Match      81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY  1 RASODIGNSL 10
    |||||:|
DB  16 RASODIGSSL 25
XX
RESULT 15
AAW95476
ID  AAW95476 standard; protein; 92 AA.
XX
AC  AAW95476;
XX
DT  29-MAR-1999 (first entry)
XX
DE  Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
XX
KW  Catalytic; antibody; phage display; immunising; phage expression vector;
XX  prodrg; scfV.
XX
OS  Mus sp.
XX
PN  US5855885-A.
XX
PD  05-JAN-1999.
XX
PF  14-JUL-1994; 94US-00273146.
XX
PR  22-JAN-1993; 93US-00007684.
XX
PA  (MCCA/) MCAFERTY J.
PA  (CHIS/) CHISWELL D.
PA  (DARS/) DARSLEY M J.
PA  (TITM/) TITMAS R C.
PA  (MART/) MARTIN M T.
PA  (KENT/) KENTEN J H.
PA  (SMIT/) SMITH R.
PA  (FITZ/) FITZGERALD K.
PA  (WILL/) WILLIAMS R O.
XX
PI  Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
PI  Kenten MH, Chiswell D, Mcafferty J, Titmas RC;
XX
XX  WPI: 1999-105036/09.
DR  N-PSDB; AAX00875.

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```

XX  Production of catalytic antibodies displayed on bacteriophages -
PR  comprises generating a gene library of antibody-derived domains inserting
PT  coding into a phage expression vector and isolating the catalytic
PR  antibodies.
XX
PS  Example 4; Fig 9A-F; 117pp; English.
XX
CC  The invention relates to methods for producing catalytic antibodies
CC  displayed on a phage. The method comprises: (a) generating a gene library
CC  of antibody-derived domains; (b) inserting coding for the domains into a
CC  phage expression vector; and (c) isolating the catalytic antibodies. The
CC  phage expression vector incorporates a histidine peptide in tandem with a
CC  myc peptide. The catalytic antibodies can be isolated by preparing an
CC  antigen; optionally immunising an animal with the antigen; generating a
CC  library of VH and VL domains from the immunised animal; cloning the VH
CC  and VL domains into a phage expression vector to generate phage display
CC  antibodies; selecting phage display antibodies which bind specifically to
CC  the antigen; screening the selected phage display antibodies for
CC  catalytic activity to substrate; and isolating the catalytic antibodies,
CC  where the phage expression vector incorporates a histidine peptide in
CC  tandem with a myc peptide. The processes are used to produce catalytic
CC  antibodies, which can be used for in vivo activation of a prodrg. The
CC  present sequence represents a genetic sequence of light chain pattern A
CC  from mouse derived RT3 phage antibodies
XX
SQ  Sequence 92 AA;
XX
Query Match      81.1%; Score 43; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY  1 RASODIGNSL 10
    |||||:|
DB  16 RASODIGSSL 25
XX
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Job time : 28.9649 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 16.2364 Seconds

(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_157_167

Perfect score: 53

Sequence: 1 RASODIGSLR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 53 | 100.0 | 243 | 9 | US-09-887-853-6 |
| 2 | 53 | 100.0 | 243 | 17 | US-10-683-547-6 |
| 3 | 53 | 100.0 | 267 | 9 | US-09-766-543-10 |
| 4 | 53 | 100.0 | 276 | 9 | US-09-766-543-12 |
| 5 | 48 | 90.6 | 109 | 14 | US-10-078-757B-55 |
| 6 | 45 | 84.9 | 112 | 14 | US-10-355-780-1 |
| 7 | 43 | 81.1 | 108 | 14 | US-10-010-729-45 |
| 8 | 43 | 81.1 | 108 | 16 | US-10-803-622-267 |
| 9 | 43 | 81.1 | 108 | 16 | US-10-803-653-267 |
| 10 | 43 | 81.1 | 109 | 9 | US-09-943-906-74 |
| 11 | 43 | 81.1 | 109 | 15 | US-10-435-602-74 |
| 12 | 43 | 81.1 | 130 | 8 | US-08-779-784-35 |
| 13 | 43 | 81.1 | 130 | 14 | US-10-010-729-71 |

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| 14 | 43 | 81.1 | 144 | 16 | US-10-642-120-4 | Sequence 4, Appl1 |
| 15 | 43 | 81.1 | 144 | 16 | US-10-642-060-4 | Sequence 4, Appl1 |
| 16 | 43 | 81.1 | 144 | 16 | US-10-642-122-4 | Sequence 4, Appl1 |
| 17 | 43 | 81.1 | 144 | 16 | US-10-642-124-4 | Sequence 4, Appl1 |
| 18 | 43 | 81.1 | 144 | 16 | US-10-621-269-4 | Sequence 4, Appl1 |
| 19 | 43 | 81.1 | 144 | 16 | US-10-620-850-4 | Sequence 4, Appl1 |
| 20 | 43 | 81.1 | 144 | 16 | US-10-642-100-4 | Sequence 4, Appl1 |
| 21 | 43 | 81.1 | 144 | 17 | US-10-642-058-4 | Sequence 4, Appl1 |
| 22 | 43 | 81.1 | 144 | 17 | US-10-642-121-4 | Sequence 4, Appl1 |
| 23 | 43 | 81.1 | 144 | 15 | US-10-239-656-55 | Sequence 55, Appl1 |
| 24 | 43 | 81.1 | 257 | 15 | US-10-239-656-67 | Sequence 67, Appl1 |
| 25 | 43 | 81.1 | 499 | 15 | US-10-239-656-73 | Sequence 73, Appl1 |
| 26 | 42 | 79.2 | 11 | 17 | US-09-155-106-4 | Sequence 4, Appl1 |
| 27 | 42 | 79.2 | 11 | 17 | US-10-808-538-4 | Sequence 4, Appl1 |
| 28 | 42 | 79.2 | 108 | 10 | US-09-155-106-22 | Sequence 22, Appl1 |
| 29 | 42 | 79.2 | 108 | 10 | US-09-155-106-23 | Sequence 23, Appl1 |
| 30 | 42 | 79.2 | 108 | 10 | US-09-155-106-24 | Sequence 24, Appl1 |
| 31 | 42 | 79.2 | 108 | 10 | US-09-155-106-28 | Sequence 28, Appl1 |
| 32 | 42 | 79.2 | 108 | 10 | US-09-155-106-30 | Sequence 30, Appl1 |
| 33 | 42 | 79.2 | 108 | 10 | US-10-808-538-22 | Sequence 22, Appl1 |
| 34 | 42 | 79.2 | 108 | 17 | US-10-808-538-23 | Sequence 23, Appl1 |
| 35 | 42 | 79.2 | 108 | 17 | US-10-808-538-24 | Sequence 24, Appl1 |
| 36 | 42 | 79.2 | 108 | 17 | US-10-808-538-28 | Sequence 28, Appl1 |
| 37 | 42 | 79.2 | 108 | 17 | US-10-808-538-30 | Sequence 30, Appl1 |
| 38 | 42 | 79.2 | 108 | 17 | US-10-808-538-49 | Sequence 49, Appl1 |
| 39 | 42 | 79.2 | 109 | 14 | US-10-078-757B-49 | Sequence 3, Appl1 |
| 40 | 39 | 73.6 | 11 | 9 | US-09-924-099-3 | Sequence 38, Appl1 |
| 41 | 39 | 73.6 | 11 | 16 | US-10-307-276B-38 | Sequence 39, Appl1 |
| 42 | 39 | 73.6 | 12 | 15 | US-10-411-869A-39 | Sequence 72, Appl1 |
| 43 | 39 | 73.6 | 31 | 9 | US-09-956-206A-3 | Sequence 72, Appl1 |
| 44 | 39 | 73.6 | 95 | 9 | US-09-943-906-72 | Sequence 72, Appl1 |
| 45 | 39 | 73.6 | 95 | 15 | US-10-435-602-72 | Sequence 72, Appl1 |

ALIGNMENTS

RESULT 1
US-09-887-853-6
Sequence 6, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
Oppermann, Hermann
Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teesta, Hurwitz & Thibault/Patent Department
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887, 853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133, 804
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 100.0%; Score 53; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
Db 157 RASODIGNSLT 167

RESULT 2
US-10-683-547-6
Sequence 6, Application US/10683547
Publication No. US20050058638A1
GENERAL INFORMATION:
APPLICANT: Houston, J.
APPLICANT: Ring, D.
APPLICANT: Oppeitman, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: CIBT-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 07/831,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 520C9 sFv
US-10-683-547-6

Query Match 100.0%; Score 53; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
Db 157 RASODIGNSLT 167

RESULT 3
US-09-766-543-10
Sequence 10, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: P01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/177,258
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10

LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 520C9
OTHER INFORMATION: humanized single-chain antibody used in the
OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 100.0%; Score 53; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
Db 176 RASODIGNSLT 186

RESULT 4
US-09-766-543-12
Sequence 12, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: P01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/177,258
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus
OTHER INFORMATION: linker
US-09-766-543-12

Query Match 100.0%; Score 53; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 11
Db 176 RASODIGNSLT 186

RESULT 5
US-10-078-757B-55
Sequence 55, Application US/10078757B
Publication No. US20030166871A1
GENERAL INFORMATION:
APPLICANT: BARBAS, Carlos F., III
APPLICANT: RADER, Christoph
TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
FILE REFERENCE: TSRI 598.0 Con1
CURRENT APPLICATION NUMBER: US/10/078,757B
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 08/986,016
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hybrid mouse - human sequence

US-10-078-757B-55

Query Match 90.6%; Score 48; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10
|||:|
Db 24 RASODIGNSL 33

RESULT 6

US-10-355-780-1
Sequence 1, Application US/10355780
Publication No. US20030143224A1
GENERAL INFORMATION:
APPLICANT: Pusineri, Stanley
APPLICANT: Safar, Jiri
APPLICANT: Williamson, Anthony
APPLICANT: Burton, Dennis
TITLE OF INVENTION: Antibodies Specific for Ungulate PrP
FILE REFERENCE: UCAL-194
CURRENT APPLICATION NUMBER: US/10/355,780
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/09/627,218B
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 112
TYPE: PrT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized peptide
US-10-355-780-1

Query Match 84.9%; Score 45; DB 14; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10
|||:|
Db 24 RASODIGNSL 33

RESULT 7

US-10-010-729-45
Sequence 45, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 45
LENGTH: 108
TYPE: PrT
ORGANISM: Mus musculus
US-10-010-729-45

Query Match 81.1%; Score 43; DB 14; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10
|||:|
Db 24 RASODIGNSL 33

RESULT 8

US-10-803-622-267
Sequence 267, Application US/10803622
Publication No. US20040157214A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogendoorn, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Jackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,622
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 267
LENGTH: 108
TYPE: PrT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain from clone MLF
US-10-803-622-267

Query Match 81.1%; Score 43; DB 16; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSL 10
|||:|

Db 24 RASQDIGSSL 33

RESULT 9
US-10-803-653-267
; Sequence 267, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 267
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain from clone M1F
US-10-803-653-267

Query Match 81.1%; Score 43; DB 16; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSSL 10
Db 24 RASQDIGSSL 33

RESULT 10
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 81.1%; Score 43; DB 9; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGSSL 10
Db 24 RASQDIGSSL 33

RESULT 11
US-10-435-602-74
; Sequence 74, Application US/10435602
; Publication No. US20030228303A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: Antibodies Specific for Native PrPsc
; FILE REFERENCE: UCAL059CON3
; CURRENT APPLICATION NUMBER: US/10/435,602
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 09/943,906
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/550,374
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 09/036,579
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 08/713,939
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: 08/528,104
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 109

TYPE: PRT
ORGANISM: mouse
US-10-435-602-74

Query Match 81.1%; Score 43; DB 15; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 12

US-08-779-784-35
Sequence 35, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-779-784-35

Query Match 81.1%; Score 43; DB 8; Length 130;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

DB 46 RASODIGSSL 55

RESULT 13

US-10-010-729-71
Sequence 71, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005C1P2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 130
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-71

Query Match 81.1%; Score 43; DB 14; Length 130;
Best Local Similarity 90.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 46 RASODIGSSL 55

RESULT 14

US-10-642-120-4
Sequence 4, Application US/10642120
Publication No. US20040131610A1
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Soares, M. Melina
APPLICANT: Ran, Sophia
TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
TITLE OF INVENTION: Antinucleoside
FILE REFERENCE: 4001.002900
CURRENT APPLICATION NUMBER: US/10/642,120
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 10/621,269
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,263
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent version 3.1
SEQ ID NO 4
LENGTH: 144
TYPE: PRT
ORGANISM: Mus musculus
US-10-642-120-4

Query Match 81.1%; Score 43; DB 16; Length 144;
Best Local Similarity 90.0%; Pred. No. 2.3;

QY 1 RASODIGNSL 10
DB 46 RASODIGSSL 55

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
|||:|
Db 46 RASQDIGSSL 55

RESULT 15

US-10-642-060-4
; Sequence 4, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibod
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-060-4

Query Match 81.1%; Score 43; DB 16; Length 144;
Best Local Similarity 90.0%; Pred. No. 2.3;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
|||:|
Db 46 RASQDIGSSL 55

Search completed: April 4, 2005, 16:42:44
Job time : 16.2364 secs

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OM protein - protein search, using 6w model

Run on: April 4, 2005, 15:32:36 ; Search time 3.97125 seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_157_167

Perfect score: 53

Sequence: 1 RASODIGNSLT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 43 | 81.1 | 88 | 2 | PI0261 Ig kappa chain V r |
| 2 | 43 | 81.1 | 106 | 2 | PI0260 Ig kappa chain V r |
| 3 | 43 | 81.1 | 130 | 1 | KVMSM4 Ig kappa chain pre |
| 4 | 42 | 79.2 | 106 | 2 | PI0259 Ig kappa chain V r |
| 5 | 41 | 77.4 | 108 | 2 | S40330 Ig kappa chain V-J |
| 6 | 39 | 73.6 | 95 | 2 | PH0865 Ig kappa chain V r |
| 7 | 38 | 71.7 | 91 | 2 | S37511 Ig kappa chain V r |
| 8 | 38 | 71.7 | 281 | 2 | S54137 probable movement |
| 9 | 37 | 69.8 | 108 | 2 | S19970 Ig kappa chain V r |
| 10 | 37 | 69.8 | 114 | 2 | S00996 Ig kappa chain pre |
| 11 | 37 | 69.8 | 125 | 2 | S40353 Ig kappa chain V-J |
| 12 | 37 | 68.8 | 127 | 2 | PH1224 Ig kappa chain pre |
| 13 | 37 | 68.8 | 312 | 2 | B96512 hypothetical prote |
| 14 | 36 | 67.9 | 53 | 2 | PH0881 Ig kappa chain V r |
| 15 | 36 | 67.9 | 93 | 2 | S38564 Ig kappa chain V r |
| 16 | 36 | 67.9 | 107 | 2 | S69901 Ig kappa chain (cl |
| 17 | 36 | 67.9 | 107 | 2 | S32188 Ig kappa chain V r |
| 18 | 36 | 67.9 | 107 | 2 | A28044 Ig kappa chain V r |
| 19 | 36 | 67.9 | 107 | 2 | D48677 Ig kappa chain V-J |
| 20 | 36 | 67.9 | 107 | 2 | B28044 Ig kappa chain V r |
| 21 | 36 | 67.9 | 107 | 2 | B49026 Ig kappa chain V r |
| 22 | 36 | 67.9 | 107 | 2 | S69906 Ig kappa chain (cl |
| 23 | 36 | 67.9 | 108 | 1 | KIHUB1 Ig kappa chain V-I |
| 24 | 36 | 67.9 | 108 | 1 | KVMSAR Ig kappa chain V r |
| 25 | 36 | 67.9 | 108 | 2 | PI0282 Ig kappa chain V r |
| 26 | 36 | 67.9 | 108 | 2 | C30502 Ig kappa chain V r |
| 27 | 36 | 67.9 | 108 | 2 | B30551 Ig kappa chain V r |
| 28 | 36 | 67.9 | 108 | 2 | C26405 Ig kappa chain V r |
| 29 | 36 | 67.9 | 108 | 2 | B26405 Ig kappa chain V r |

| | | | | | |
|----|----|------|-----|---|---------------------------|
| 30 | 36 | 67.9 | 108 | 2 | S38862 Ig kappa chain V r |
| 31 | 36 | 67.9 | 108 | 2 | S69902 Ig kappa chain (cl |
| 32 | 36 | 67.9 | 108 | 2 | S69900 Ig kappa chain (cl |
| 33 | 36 | 67.9 | 108 | 2 | S69903 Ig kappa chain (cl |
| 34 | 36 | 67.9 | 115 | 2 | A53276 Ig kappa chain V r |
| 35 | 36 | 67.9 | 115 | 2 | JL0080 Ig kappa chain pre |
| 36 | 36 | 67.9 | 122 | 2 | A29380 Ig kappa chain pre |
| 37 | 36 | 67.9 | 126 | 2 | A34904 Ig kappa chain pre |
| 38 | 36 | 67.9 | 128 | 2 | A28406 Ig kappa chain V r |
| 39 | 36 | 67.9 | 298 | 2 | B75429 hypothetical prote |
| 40 | 36 | 67.9 | 730 | 2 | B83592 Ig kappa chain pre |
| 41 | 35 | 66.0 | 125 | 2 | S04936 Ig kappa chain pre |
| 42 | 35 | 66.0 | 130 | 2 | PI0113 Ig kappa chain pre |
| 43 | 35 | 66.0 | 139 | 2 | S40365 Ig kappa chain h |
| 44 | 35 | 66.0 | 422 | 1 | KKHUZ plasma protein 2 p |
| 45 | 34 | 64.2 | 87 | 2 | PH1082 Ig light chain V r |

ALIGNMENTS

RESULT 1
PI0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C/Accession: PI0261
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PI0231; MUID:90111618; PMID:2104919
A/Accession: PI0261
A/Molecule type: mRNA
A/Residues: 1-88 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:1-5/Region: framework 1
F:6-16/Region: complementarity-determining 1
F:17-31/Region: framework 2
F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match 81.1%; Score 43; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSLT 10
DB 6 RASODIGSL 15

RESULT 2
PI0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletscky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PI0231; MUID:90111618; PMID:2104919
A/Accession: PI0260
A/Molecule type: mRNA
A/Residues: 1-106 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMW>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 81.1%; Score 43; DB 2; Length 106;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 3

KVMSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N/Contains: Ig kappa chain precursor V region VK41
C/Species: Mus musculus (house mouse)
C/Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text change 09-Jul-2004
C/Accession: A93211; B93211; A93815; A94239; A01922; A01923
R/Seidman, J.G.; Max, E.E.; Leder, P.

Nature 280, 370-375, 1979
A/Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A/Reference number: A93211; MUID:79221900; PMID:111146

A/Accession: A93211

A/Molecule type: DNA

A/Residues: 1-130 <PC41>

A/Cross-references: UNIPROT:P01639

A/Accession: B93211

A/Molecule type: DNA

A/Residues: 1-117 <VK41>

A/Cross-references: GB:J00804; GB:J00566; NID:952127; PIDN:CA24186.1; PID:9575660

A/Note: the sequences were determined from the differentiated gene MOPC 41 and the germi

R/Buretein, V.; Schacher, I.

Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A/Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor

A/Reference number: A93815; MUID:77148916; PMID:403522

A/Accession: A93815

A/Molecule type: protein

A/Residues: 1-33 <BUR>

A/Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R/Gray, W.R.; Dreyer, W.J.; Hood, L.

Science 155, 465-467, 1967

A/Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A/Reference number: A94239; MUID:67056897; PMID:4162931

A/Accession: A94239

A/Molecule type: protein

A/Residues: 23-49; B'51-53; 'USB', 57-58; 'ZZ', 61-62; 'BZ', 65-76; 'B', 78-108; 110-130 <GRA>

A/Experimental source: Bence Jones protein MOPC 41

C/Genetics:

A/Introns: 19/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: alternative initiators; heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status experimental <SIG1>

F:3-22/Domain: signal sequence #status experimental <SIG2>

F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match 81.1%; Score 43; DB 1; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 46 RASODIGSSL 55

RESULT 4

PL0259
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 21-Jan-2000
C/Accession: PL0259

R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletschy, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A/Reference number: PL0231; MUID:90111618; PMID:2104919

A/Accession: PL0259

A/Molecule type: mRNA

A/Residues: 1-106 <SHL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 79.2%; Score 42; DB 2; Length 106;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 24 RASODIGSSL 33

RESULT 5

S40330
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence revision 26-May-1995 #text change 23-Jul-1999
C/Accession: S40330
R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40330

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-108 <KLE>

A/Cross-references: EMBL:X72440; NID:9441348; PIDN:CA51108.1; PID:9441349

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 41; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASODIGNSL 10
DB 27 RASODIGSSL 36

RESULT 6

PH0865
Ig kappa chain V region (anti-DNA, I-2a) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text change 21-Jan-2000
C/Accession: PH0865

R/Mahelner-Loty, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0865

A/Molecule type: DNA

A/Residues: 1-95 <MAN>

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-23/Region: framework 1
F/16-90/Domain: immunoglobulin homology <IMM>
F/24-34/Region: complementarity-determining 1
F/35-49/Region: framework 2
F/50-56/Region: complementarity-determining 2
F/57-88/Region: framework 3
F/89-95/Region: complementarity-determining 3

Query Match 73.6%; Score 39; DB 2; Length 95;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RASQDIGNSLT 11
||| ||| |||
Db 24 RASQDINRYLT 34

RESULT 7
837511
Ig kappa chain V region (V-kappa 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37511
R/Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Accession: S37511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-91 <KLE>
A/Cross-references: EMBL:226600; NID:g405664; PIDD:CAA81354.1; PID:g405665
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 38; DB 2; Length 91;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNSL 10
||| ||| |||
Db 7 RASQSVGNL 16

RESULT 8
554137
probable movement protein - asparagus virus II
C/Species: asparagus virus II
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 03-Jul-2004
C/Accession: S54137
R/Rafael-Martin, M.; Rivera-Bustamante, R.F.
submitted to the EMBL Data Library, April 1995
A/Description: Nucleotide sequence of asparagus virus II (AVII) RNA3.
A/Reference number: S54137
A/Accession: S54137
A/Molecule type: genomic RNA
A/Residues: 1-281 <RAE>
A/Cross-references: UNIPROT:Q65298; EMBL:X86352; NID:g807865; PIDD:CAA60124.1; PID:g8089
A/Experimental source: isolate Mexican
C/Superfamily: alfalfa mosaic virus 32.4K protein

Query Match 71.7%; Score 38; DB 2; Length 281;
Best Local Similarity 63.6%; Pred. No. 6.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNSLT 11
||| ||| |||
Db 176 RYSEDEVGSSLT 186

RESULT 9
51970
Ig kappa chain V region (V-T151) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S1970
R/Weissenhorn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A/Description: Structural characterization of CD4 mAb.
A/Reference number: S19963
A/Accession: S19970
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <WEI>
A/Cross-references: EMBL:X65095; NID:g52286; PIDD:CAA46223.1; PID:g52287
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 4;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RASQDIGNSLT 11
||| ||| |||
Db 24 RASQDINRYLT 34

RESULT 10
S00996
Ig kappa chain precursor V region (A10) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
C/Accession: S00996
R/Strubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.
Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A/Title: Two unusual human immunoglobulin V-kappa genes.
A/Reference number: S00996; MUID:89134397; PMID:2852016
A/Accession: S00996
A/Molecule type: DNA
A/Residues: 1-114 <STR>
A/Cross-references: EMBL:M27750; NID:g185914; PIDD:AAA5912.1; PID:g553479
A/Note: this sequence was determined from the germline gene
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-114/Product: Ig kappa chain V region #status predicted <MAT>
F/42-107/Disulfide bonds: #status predicted

Query Match 69.8%; Score 37; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNSL 10
||| ||| |||
Db 43 RASQSIGSSL 52

RESULT 11
S40353
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40353
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40353
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-125 <KLE>
A/Cross-references: EMBL:X72463
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 38 RASQDIGNSL 47

RESULT 12

PH1224
Ig kappa chain precursor V region (M-T151) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000

C:Accession: PH1224

R:Weissenborn, W.; Scheuer, W.; Kaluza, B.; Schwitzke, M.; Reiter, C.; Flieger, D.; Lenz
Gene 121, 271-278, 1992

A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
A:Reference number: PH1224; MWID:93077041; PMID:1446824

A:Accession: PH1224

A:Molecule type: mRNA

A:Residues: 1-127 <WEI>
A:Cross-references: GB:S50261; NID:g260761; PIDN:AAB24318.1; PID:g260762

A>Note: this mouse sequence was hybridized and fused with a human constant region gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-127/Product: Ig light chain V region #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 37; DB 2; Length 127;
Best Local Similarity 72.7%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 11
DB 44 RASQDIGNSL 54

RESULT 13

B96512
Hypothetical protein P2G19.20 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: B96512

R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Naseen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Galzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MWID:21016719; PMID:11130712

A:Accession: B96512

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-312 <STO>

A:Cross-references: UNIPROT:Q9C628; GB:AE005173; NID:g11321767; PIDN:AAG34244.1; GSPDB:C

C:Genetics:
A:Gene: P2G19.20
A:Map position: 1

Query Match 69.8%; Score 37; DB 2; Length 312;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10

DB 289 KVSRDIGNSL 298

RESULT 14

PH0881
Ig kappa chain V region (GOU) - human (fragment)

N:Alternate names: myeloma protein
C:Species: Homo sapiens (man)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C:Accession: PH0881

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosesein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
A:Reference number: PH0881; MWID:92078875; PMID:160528

A:Accession: PH0881

A:Molecule type: protein

A:Residues: 1-53 <MAN>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1

F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2

F:50-53/Region: complementarity-determining 2

Query Match 67.9%; Score 36; DB 2; Length 53;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 24 RASQDIGNSL 33

RESULT 15

S38564
Ig kappa chain V region (ASWU1) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S38564

R:Monestier, M.; Losman, L.J.; Novick, K.E.; Arleb, J.P.
submitted to the EMBL Data Library, September 1993

A:Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s Mj

A:Reference number: S38559

A:Accession: S38564

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <MON>

A:Cross-references: EMBL:X75105; NID:g414153; PIDN:CAA52996.1; PID:g414154
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 36; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 24 RASQDIGNSL 33

Search completed: April 4, 2005, 15:58:01
Job time : 4.97125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 18.5911 seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_157_167
Perfect score: 53
Sequence: 1 RASODIGNSLT 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 43 | 81.1 | 130 | 1 | KV5G_MOUSE |
| 2 | 40 | 75.5 | 365 | 2 | Q65SM6 |
| 3 | 38 | 71.7 | 281 | 2 | Q65298 |
| 4 | 38 | 71.7 | 283 | 2 | Q98702 |
| 5 | 38 | 71.7 | 283 | 2 | Q91MN5 |
| 6 | 37 | 69.8 | 312 | 2 | Q9C628 |
| 7 | 37 | 69.8 | 447 | 2 | Q6R6C8 |
| 8 | 37 | 69.8 | 4091 | 2 | Q7QA48 |
| 9 | 36 | 67.9 | 108 | 1 | KVIC_HUMAN |
| 10 | 36 | 67.9 | 108 | 1 | KV5K_MOUSE |
| 11 | 36 | 67.9 | 108 | 1 | KV5L_MOUSE |
| 12 | 36 | 67.9 | 108 | 1 | KV5M_MOUSE |
| 13 | 36 | 67.9 | 108 | 1 | KV5N_MOUSE |
| 14 | 36 | 67.9 | 108 | 1 | KV5O_MOUSE |
| 15 | 36 | 67.9 | 127 | 2 | Q925S9 |
| 16 | 36 | 67.9 | 133 | 2 | Q6CRP8 |
| 17 | 36 | 67.9 | 236 | 2 | Q7Z3Y4 |
| 18 | 36 | 67.9 | 288 | 1 | Q6MMU3 |
| 19 | 36 | 67.9 | 298 | 1 | UB72_DEIRA |
| 20 | 36 | 67.9 | 423 | 2 | Q6R6T3 |
| 21 | 36 | 67.9 | 515 | 2 | Q9FVDS |
| 22 | 36 | 67.9 | 730 | 2 | Q91683 |
| 23 | 36 | 67.9 | 1222 | 2 | Q87XK8 |
| 24 | 35 | 66.0 | 133 | 2 | Q9QOV6 |
| 25 | 35 | 66.0 | 166 | 2 | Q7WZP4 |
| 26 | 35 | 66.0 | 236 | 2 | Q6GFP1 |
| 27 | 35 | 66.0 | 282 | 2 | Q57164 |
| 28 | 35 | 66.0 | 283 | 2 | O11876 |
| 29 | 35 | 66.0 | 339 | 2 | Q7MDBO |
| 30 | 35 | 66.0 | 342 | 1 | MURB_RALSO |
| 31 | 35 | 66.0 | 348 | 2 | Q8D6F5 |

| | | | | | | |
|----|----|------|------|---|------------|---------------------|
| 32 | 35 | 66.0 | 349 | 2 | Q87IS9 | Q87IS9 vibrrio para |
| 33 | 35 | 66.0 | 374 | 2 | O05107 | O05107 ectothiorho |
| 34 | 35 | 66.0 | 400 | 1 | PRTZ_HUMAN | P22891 homo sapien |
| 35 | 35 | 66.0 | 490 | 2 | Q8PDC1 | Q8PDC1 xanthomonas |
| 36 | 35 | 66.0 | 535 | 2 | Q822S9 | Q822S9 chlamydomo |
| 37 | 35 | 66.0 | 867 | 2 | Q8XCF2 | Q8XCF2 neurospora |
| 38 | 35 | 66.0 | 1134 | 2 | Q7YVE0 | Q7YVE0 cryptospori |
| 39 | 35 | 66.0 | 1338 | 2 | Q75JG1 | Q75JG1 dictyostell |
| 40 | 34 | 64.2 | 81 | 2 | Q9NPB5 | Q9NPB5 homo sapien |
| 41 | 34 | 64.2 | 108 | 1 | KVIC_HUMAN | P01599 homo sapien |
| 42 | 34 | 64.2 | 108 | 1 | KVIC_HUMAN | P01610 homo sapien |
| 43 | 34 | 64.2 | 115 | 1 | KV5I_MOUSE | P01642 mus musculu |
| 44 | 34 | 64.2 | 199 | 2 | Q65VU1 | Q65VU1 manheimia |
| 45 | 34 | 64.2 | 257 | 2 | Q62HW0 | Q62HW0 burkholderi |

ALIGNMENTS

| RESULT 1 | KV5G_MOUSE | STANDARD; | PRT; | 130 AA. |
|----------|--|-----------------|------|------------------------------------|
| ID | KV5G_MOUSE | P01639; P01640; | | |
| AC | P01639; P01640; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Ig kappa chain V-V region MOPC 41 precursor. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_Taxid=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=79221900; PubMed=111146; | | | |
| RA | Seldman J.G., Max E.E., Leder P.; | | | |
| RT | "A kappa-immunoglobulin gene is formed by site-specific recombination | | | |
| RT | without further somatic mutation."; | | | |
| RL | Nature 280:370-375 (1979). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 1-33. | | | |
| RX | MEDLINE=77148916; PubMed=403522; | | | |
| RA | Buretein Y., Schechter I.; | | | |
| RT | "Amino acid sequence of the NH2-terminal extra piece segments of the | | | |
| RT | precursors of mouse immunoglobulin lambda1-c type and kappa-type light | | | |
| RL | chains."; | | | |
| RN | [3] | | | |
| RP | Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977). | | | |
| RX | SEQUENCE OF 23-130. | | | |
| RA | MEDLINE=67056897; PubMed=4162911; | | | |
| RT | Gray W.R., Dreyer W.U., Hood L.; | | | |
| RT | "Mechanism of antibody synthesis: size differences between mouse kappa | | | |
| RL | chains."; | | | |
| CC | Science 155:465-467(1967). | | | |
| CC | -I- MISCELLANEOUS: This precursor was synthesized in a cell-free | | | |
| CC | system directed by mRNA isolated from myeloma polyosomes. | | | |
| CC | -I- MISCELLANEOUS: This is a Bence-Jones protein. | | | |
| CC | PIR; A93211; KVM5M4. | | | |
| DR | HSSP; P01594; JLV5. | | | |
| DR | InterPro; IPR007110; Ig-like. | | | |
| DR | InterPro; IPR003596; Ig_v. | | | |
| DR | Pfam; PF00047; Ig_1. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |
| DR | PROSITE; PS50835; IG_LIKE; 1. | | | |
| KW | Bence-Jones protein; Direct protein sequencing; | | | |
| KW | Immunoglobulin V region; Signal. | | | |
| FT | SIGNAL | 1 | 22 | |
| FT | CHAIN | 23 | 130 | Ig kappa chain V-V region MOPC 41. |
| FT | DOMAIN | 23 | 45 | Framework-1. |
| FT | DOMAIN | 46 | 56 | Complementarity-determining-1. |
| FT | DOMAIN | 57 | 71 | Framework-2. |
| FT | DOMAIN | 72 | 78 | Complementarity-determining-2. |
| FT | DOMAIN | 79 | 110 | Framework-3. |
| FT | DOMAIN | 111 | 119 | Complementarity-determining-3. |

FT DOMAIN 120 129 Framework-4.
 FT DISUPRID 45 110 By similarity.
 FT VARIANT 1 2 Missing (in 25% of the molecules).
 FT NON_TER 130 130
 SO SEQUENCE 130 AA; 14311 MW; 5E9E0FE71D5F1BEC CRC64;

Query Match 81.1%; Score 43; DB 1; Length 130;
 Best Local Similarity 90.0%; Pred. No. 1.5;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 10
 |||||
 Db 46 RASODIGSSL 55

RESULT 2
 ID O65SW6 PRELIMINARY; PRT; 365 AA.
 AC O65SW6;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE OmpC protein.
 GN Name=ompC; ORFNames=MS1337;
 OS Mannheimia succiniciproducens MBE155E.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 NC NCBI_TaxId=221988;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MBE155E;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.,
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 succiniciproducens.";
 RL Nat. Biotechnol. 0:0-0(2004).
 DR EMBL; AE016827; AAU37944.1; -.
 SO SEQUENCE 365 AA; 40255 MW; 83DD67AF0F30BF27 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 365;
 Best Local Similarity 63.6%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11
 :|||:|
 Db 65 KASODIGNLS 75

RESULT 3
 ID O65298 PRELIMINARY; PRT; 281 AA.
 AC O65298;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Putative movement protein.
 GN Name=ORP1;
 OS Asparagus virus 2.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
 OC Ilarvirus.
 NC NCBI_TaxId=39681;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Rafael-Martin M., Rivera-Bustamante R.F.,
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X86352; CAA60124.1; -.
 DR PIR; S54137; S54137.
 DR InterPro; IPR002538; Bromo_MP.
 DR Pfam; PF01573; Bromo_MP; 1_
 SO SEQUENCE 281 AA; 31476 MW; 891B345872FC2E25 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 281;
 Best Local Similarity 63.6%; Pred. No. 36;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RASODIGNSLT 11
 |||||
 Db 176 RYSEDVGSST 186

RESULT 4
 ID Q98702 PRELIMINARY; PRT; 283 AA.
 AC Q98702;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Movement protein.
 OS Elm mottle virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
 OC Ilarvirus.
 NC NCBI_TaxId=56486;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97372954; PubMed=9229009;
 RA Ge X., Scott S.W., Zimmerman M.T.,
 RT "The complete sequence of the genomic RNAs of spinach latent virus.";
 RL Arch. Virol. 142:1213-1226(1997).
 DR EMBL; U57048; AA897770.1; -.
 DR InterPro; IPR002538; Bromo_MP.
 DR Pfam; PF01573; Bromo_MP; 1_
 SO SEQUENCE 283 AA; 31508 MW; 9D3B923A8748BB6A CRC64;

Query Match 71.7%; Score 38; DB 2; Length 283;
 Best Local Similarity 63.6%; Pred. No. 36;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11
 |||||
 Db 176 RYSEDVGSST 186

RESULT 5
 ID Q91MN5 PRELIMINARY; PRT; 283 AA.
 AC Q91MN5;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Putative movement protein 3a.
 OS Hydrangea mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
 OC Ilarvirus.
 NC NCBI_TaxId=42812;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22897981; PubMed=14551826;
 RA Scott S.W., Zimmerman M.T., Ge X.,
 RT "Viruses in subgroup 2 of the genus Ilarvirus share both serological
 RT relationships and characteristics at the molecular level.";
 RL Arch. Virol. 148:2063-2075(2003).
 DR EMBL; AF172965; AAF89807.1; -.
 DR InterPro; IPR002538; Bromo_MP.
 DR Pfam; PF01573; Bromo_MP; 1_
 SO SEQUENCE 283 AA; 31508 MW; 863CD623774291A5 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 283;
 Best Local Similarity 63.6%; Pred. No. 36;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASODIGNSLT 11
 |||||
 Db 176 RYSEDVGSST 186

RESULT 6

09C628 PRELIMINARY; PRT; 312 AA.
ID 09C628
AC 09C628
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein F2G19.20.
GN Name=F2G19.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Rongling C.M., Xoo H., Fujii C.Y., Utecherback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC083835; AAC50622.1; -.
DR PIR; B96512; B96512.
DR InterPro; IPR006527; F_box_assoc.1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 36256 MW; 025F1B0740BFP940 CRC64;
Query Match 69.8%; Score 37; DB 2; Length 312;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 1 RASODIGNSLT 10
Db 289 KVSRDIGNSLT 298
RESULT 7
06R6C8 PRELIMINARY; PRT; 847 AA.
ID 06R6C8
AC 06R6C8
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AcTA.
GN Name=acTA;
OS Listeria Ivanovii subsp. londoniensis.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=202752;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NRL 33021;
RA Ward T.J., Gorski L., Bornucki M.K., Mandrell R.E., Hutchins J.,
RA Pupedis K.;
RT "Interspecific Phylogeny and Lineage Group Identification Based on the
RT prfA Virulence Gene Cluster of Listeria monocytogenes.";
RL J. Bacteriol. 186:4994-5002(2004).
DR EMBL; AY510073; AAR97354.1; -.
DR InterPro; IPR007752; AcTA.
DR Pfam; PF05058; AcTA; 1.
SQ SEQUENCE 847 AA; 92364 MW; D9B407E0F5A813 CRC64;
Query Match 69.8%; Score 37; DB 2; Length 847;
Best Local Similarity 45.5%; Pred. No. 19e+02;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
CY 1 RASODIGNSLT 11
Db 811 KANOEVENNMT 821
RESULT 8
07QA48 PRELIMINARY; PRT; 4091 AA.
ID 07QA48
AC 07QA48

DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AGCP14079 (Fragment).
GN Name=agCG48186; ORFNames=ENSANG00000014545;
OS Anopheles gambiae str. PEST.
OC Anopheles; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100898; EAA09222.1; -.
DR HSRP; Q01082; IBER.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00019; SH3_1; 1.
DR Pfam; PF00435; Spectrin_31.
DR PRINTS; PRO0683; SPECTRINPH.
DR PRODOM; PD000066; SH3; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS00021; CH; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00002; SH3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW SH3 domain.
FT NON_TER 1 1
FT 4091 4091
SQ SEQUENCE 4091 AA; 469663 MW; B123C7AA94B9D8B CRC64;
Query Match 69.8%; Score 37; DB 2; Length 4091;
Best Local Similarity 70.0%; Pred. No. 9.9e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 2 ASODIGNSLT 11
Db 3038 ASKDSLSLT 3047
RESULT 9
KVIC_HUMAN STANDARD; PRT; 108 AA.
ID KVIC_HUMAN
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RX Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT Bi). 3. The complete amino acid sequence and the genetic significance

RT of the variability principles for the mechanism of antibody formation."
 RT Hoppe-Sejler's Z. Physiol. Chem. 353:1284-1306(1972).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01863; KIHUBI.
 DR HSP; P01607; IBMV.
 DR GO; GO:0005576; C-reactive protein; NMS.
 DR GO; GO:0003823; Antigen binding; NMS.
 DR GO; GO:0006955; P:immune response; NMS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 AC P01645; Complementarity-determining-1.
 DT 21-JUL-1986 (Rel. 01, Created)
 FT DOMAIN 35 49 Framework-2.
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;
 Best Local Similarity 80.0%; Pred. No. 33;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
 DB 24 RASODIRNSL 33

RESULT 10
 KVSX MOUSE
 ID KVSX MOUSE STANDARD; PRT; 108 AA.
 AC P01644;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP R16.7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
 RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 CC PIR; A01927; KVSAR.
 DR HSP; P01594; IJVS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 AC P01646; Complementarity-determining-1.
 DT 21-JUL-1986 (Rel. 01, Created)
 FT DOMAIN 35 49 Framework-2.
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 108 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFP597 CRC64;
 Query Match 67.9%; Score 36; DB 1; Length 108;
 Best Local Similarity 80.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
 DB 24 RASODIRNSL 33

RESULT 11
 KVSX MOUSE
 ID KVSX MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
 RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 CC HSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 AC P01646; Complementarity-determining-1.
 DT 21-JUL-1986 (Rel. 01, Created)
 FT DOMAIN 35 49 Framework-2.
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 108 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFP58B CRC64;
 Query Match 67.9%; Score 36; DB 1; Length 108;
 Best Local Similarity 80.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
 KVSX MOUSE
 ID KVSX MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP 123B6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RA MEDLINE=82150934; PubMed=6801658;
RT "Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BBA09A CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
DB 24 RASODISNYL 33

RESULT 13
ID KVSX MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124B1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RA MEDLINE=82150934; PubMed=6801658;
RT "Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; IRET.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;

FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653BEEFA2 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
DB 24 RASODINNYL 33

RESULT 14
ID KVSQ MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RA MEDLINE=82150934; PubMed=6801658;
RT "Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01594; 1JVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;

Query Match 67.9%; Score 36; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASODIGNSL 10
DB 24 RASODINNYL 33

RESULT 15
ID Q925S9 PRELIMINARY; PRT; 127 AA.
AC Q925S9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Foan K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF";
RL Hybridoma 18:193-202(1999).
DR EMBL; AF124721; AK55120.1; -.
DR HSSP; P01594; IJVS.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 127 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BBB981FA5 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 127;
Best Local Similarity 80.0%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
DB 44 RASQDIGINL 53

Search completed: April 4, 2005, 15:56:08
Job time : 20.5911 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 13.9776 seconds

(without alignment)
193.690 Million cell updates/sec

Title: US-09-887-853-6_COPY_183_189

Perfect score: 31

Sequence: 1 ATSSLDs 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneeqp1980a:*
2: geneeqp1990a:*
3: geneeqp2000a:*
4: geneeqp2001a:*
5: geneeqp2002a:*
6: geneeqp2003a:*
7: geneeqp2004a:*
8: geneeqp2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 2 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 3 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 4 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 5 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 6 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 7 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 8 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 9 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 10 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 11 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 12 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 13 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 14 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 15 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 16 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 17 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 18 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 19 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 20 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 21 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 22 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 23 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 24 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |
| 25 | 31 | 100.0 | 7 | AAW70945 | AAW70945 CDR2 of t |

| | | | | | | |
|----|----|-------|-----|---|----------|--------------------|
| 26 | 31 | 100.0 | 109 | 2 | AAW18271 | AAW18271 PRP 37 11 |
| 27 | 31 | 100.0 | 109 | 2 | AAW65910 | AAW65910 PRP 37 11 |
| 28 | 31 | 100.0 | 109 | 2 | AAW65910 | AAW65910 PRP 37 11 |
| 29 | 31 | 100.0 | 109 | 5 | AAW51796 | AAW51796 Anti-PRP |
| 30 | 31 | 100.0 | 109 | 6 | AAW58877 | AAW58877 Anti-PRP |
| 31 | 31 | 100.0 | 109 | 8 | AAW10235 | AAW10235 Murine an |
| 32 | 31 | 100.0 | 112 | 5 | AAW50879 | AAW50879 Anti-bov |
| 33 | 31 | 100.0 | 129 | 6 | AAW55323 | AAW55323 Amino aci |
| 34 | 31 | 100.0 | 130 | 8 | AAW12651 | AAW12651 Human ant |
| 35 | 31 | 100.0 | 135 | 3 | AAW44599 | AAW44599 Mouse lig |
| 36 | 31 | 100.0 | 144 | 8 | AAW57086 | AAW57086 3G4 antib |
| 37 | 31 | 100.0 | 146 | 1 | AAW30251 | AAW30251 Sequence |
| 38 | 31 | 100.0 | 147 | 4 | AAW55566 | AAW55566 Human col |
| 39 | 31 | 100.0 | 153 | 8 | AAW57089 | AAW57089 3G4-2BVL |
| 40 | 31 | 100.0 | 234 | 6 | AAW26968 | AAW26968 Bacterial |
| 41 | 31 | 100.0 | 235 | 6 | AAW55322 | AAW55322 Amino aci |
| 42 | 31 | 100.0 | 237 | 3 | AAW44595 | AAW44595 EGFV#125 |
| 43 | 31 | 100.0 | 243 | 2 | AAW02280 | AAW02280 520C9 ant |
| 44 | 31 | 100.0 | 243 | 2 | AAW53170 | AAW53170 520C9 ant |
| 45 | 31 | 100.0 | 243 | 2 | AAW80424 | AAW80424 520C9 PRV |

ALIGNMENTS

RESULT 1
AAW70945 standard; peptide: 7 AA.
ID AAW70945; (first entry)
AC AAW70945; (first entry)
DT 14-OCT-1998 (first entry)
DE CDR2 of the light chain of monoclonal antibody RS-255.
XX pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
XX respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
XX viral infection; inhibit; fusion; protection; transfection;
XX antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX Synthetic.
OS Mus sp.
OS FR2758331-AL.
PN 17-JUL-1998.
PD 14-JAN-1997; 97FR-00000300.
XX 14-JAN-1997; 97FR-00000300.
XX (UYBO-) UNIV BOURGOGNE.
XX WPI; 1998-390320/34.
PT New peptide(s) recognising viral epitope with tropism to mucosa - useful for, e.g. diagnosing, preventing and treating viral infection(s).
PS Claim 12; Page 39; 51pp; French.
CC AAW70905-46 represent peptide sequences that can recognise, by antigen-antibody type reactions, at least 1 epitope of a pathogenic virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR regions of monoclonal antibodies specific for respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies specific for site III or IV of the VP6 protein of rota virus (RV). The peptides can neutralise viral infections and may also inhibit fusion between infected and uninfected cells or cells and viruses. They provide passive or active protection and/or inhibit transfection of the virus, so are useful as antiviral agents or for prophylaxis, in human or veterinary medicine. The peptides can be labelled and used to diagnose infection or contamination by the virus. The peptides are particularly directed against RSV or RS but may also be used against papilloma, adeno,

CC entero, polio, influenza or immune deficiency viruses
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 1 ATSSIDS 7

RESULT 2
AAV44590

ID AAV44590 standard; protein; 7 AA.

AC AAV44590;

DT 04-APR-2000 (first entry)

DE Mouse anti-IL-18 antibody VL complementarity-determining region-2.

XX Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KM complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KM monoclonal antibody #125-2Hmab; interleukin-18; antiinflammatory;
KM immunosuppressive; leucocytopenic; antiallergic; antipyretic;
KM antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KM inflammatory disorder; immunoreaction.

XX Mus musculus.

OS BP974600-A2.

PN 26-JUN-2000.

PF 24-JUN-1999; 99EP-00304977.

PR 24-JUN-1998; 98JP-00177580.

PR 12-OCT-1998; 98JP-00289044.

PR 22-DEC-1998; 98JP-00365023.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

PI WPI; 2000-118341/11.

DR N-PSDB; AA249537.

XX New artificially produced peptide for neutralizing biological activity of
PT interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases.

PS Claim 7, Page 18, 32pp; English.

XX The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-interleukin-18 antibody light chain variable region
CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2Hmab, which is capable of neutralizing biological activities of
CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
CC leucocytopenic, antiallergic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7

DB 1 ATSSIDS 7

RESULT 3
ABR55316
ID ABR55316 standard; peptide; 7 AA.

AC ABR55316;

DT 29-JUL-2003 (first entry)

DE Complementarity determining region of light chain of antibody VR165.

XX Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;
KM complementarity determining region; vascular endothelial growth factor;
KM CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.

OS Mus sp.

PN WO2003031475-A2.

PD 17-APR-2003.

PF 10-OCT-2002; 2002WO-GB004619.

PR 10-OCT-2001; 2001GB-00024317.

PA (CELL-) CELLTECH R & D LTD.

PI Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;

DR WPI; 2003-441133/41.

XX Novel antibody molecules having specificity for human kinase insert
PT domain-containing receptors, useful for treating inflammation, psoriasis,
PT rheumatoid arthritis, tumor growth and metastasis.

PS Claim 2; Fig 1; 57pp; English.

XX The specification describes an antibody molecule which has specificity
CC for human kinase insert domain-containing receptor (KDR). The antibody
CC comprises complementarity determining regions (CDRs) from the heavy and
CC light chain variable domains of the murine monoclonal antibody VR165.
CC This antibody is specific for human KDR. The antibody of the invention
CC blocks vascular endothelial growth factor (VEGF) binding to KDR.
CC Antibodies of the invention are useful for treating a pathology in which
CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
CC growth or metastasis. ABR55315-17 represent the CDRs of the light chain
CC variable region of VR165 antibody. They are used to produce antibodies of
CC the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 1 ATSSIDS 7

RESULT 4

ID ADM78136
ADM78136 standard; peptide; 7 AA.

AC ADM78136;

DT 01-JUL-2004 (first entry)

DE Human 5JB3-86 antibody variable light chain CDR2 peptide region.
 XX
 KM monoclonal antibody; adenylate kinase isozyme 3;
 KM complementarity determining region; CDR; heart disease; marker AK3;
 KM biochemical; human; variable; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004029094-A1.
 XX
 PD 08-APR-2004.
 XX
 PF 27-SEP-2003; 2003WO-KR001979.
 XX
 PR 28-SEP-2002; 2002KR-00059211.
 XX
 PA (KIMH/) KIM H.
 XX
 PI KIm H;
 XX
 DR WPI; 2004-316088/29.
 XX
 PT New monoclonal antibody specific to human mitochondrial adenylate kinase
 PT isozyme 3, useful for preparing a composition for detecting a heart
 PT disease marker AK3.
 XX
 PS Claim 1; SEQ ID NO 99; 126pp; English.
 XX
 CC The invention relates to a novel monoclonal antibody specific to
 CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity
 CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
 CC invention further relates to: a composition comprising the monoclonal
 CC antibody for detecting a heart disease marker AK3; a kit comprising the
 CC monoclonal antibody for the diagnosis of heart disease; and a method of
 CC detecting a heart disease marker AK3. The monoclonal antibody is useful
 CC for preparing a composition for detecting a heart disease marker AK3. The
 CC monoclonal antibody reduces false positive results of the conventional
 CC biochemical markers. This sequence represents a human antibody variable
 CC light chain CDR peptide region of the invention.
 CC
 SQ Sequence 7 AA;
 QY
 DB 1 ATSSLDS 7
 1 ATSSLDS 7
 1 ATSSLDS 7
 Query Match 100.0%; Score 31; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 27-NOV-2002; 2002US-00307276.
 XX
 XX 27-NOV-2002; 2002US-00307276.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Partridge WM, Bado RJ;
 XX
 DR WPI; 2004-459888/43.
 XX
 PD Humanized murine antibody that bind to human insulin receptor useful to
 PT transport neuropharmaceutical agents; has heavy and light amino acid
 PT chain having complementarity determining regions interspersed between
 PT humanized framework regions.
 XX
 XX Claim 2; SEQ ID NO 40; 34pp; English.
 XX
 PS The invention describes a humanised antibody (I) that binds with the
 XX human insulin receptor (HIR). The humanised antibody comprises a heavy
 XX chain of amino acids comprising a constant region and a variable region
 XX where the variable region has an amino end and a carboxyl end and
 XX comprises complementarity determining regions (CDR) interspersed between
 XX framework regions, the CDR comprises a first CDR located at the amino end
 XX of the variable region, a third CDR located at the carboxyl end of the
 XX variable region and a second CDR located between the first and third
 XX CDRs. The framework regions comprise a first frame work region located
 XX adjacent to the amino end of the first CDR, a second framework region
 XX located between the first and second CDR, a third frame work region
 XX located between the second and third CDR and a fourth frame work region
 XX located adjacent to the carboxyl end of the third CDR, where the
 XX framework regions have been humanized, and a light chain of aminoacids
 XX compatible with the heavy chain. (I) is useful for increasing the ability
 XX of neuropharmaceutical agent to cross the human blood brain barrier which
 XX involves linking the neuropharmaceutical agent to (I) by an avidin-biotin
 XX linkage or by genetic fusion. (I) is useful for targeting a
 XX pharmaceutical agent to the HIR in vivo which involves linking the
 XX pharmaceutical agent to (I). A preparation (II) comprising (I) is useful
 XX for intravenously administering a pharmaceutical agent to a human patient
 XX which involves injecting (II) into blood stream of the human patient. (I)
 XX is useful in combination with drug and diagnostic agent to treat human
 XX beings in vivo. (I) is useful as Trojan horse to transport
 XX neuropharmaceutical agents across blood brain barrier. This is the amino
 XX acid sequence of mouse antibody 83-14 light chain complementarity
 XX determining region 2 (CDR2), showing the preferred sequence of the CDR
 XX within the humanised antibody.
 SQ Sequence 7 AA;
 QY
 DB 1 ATSSLDS 7
 1 ATSSLDS 7
 1 ATSSLDS 7
 Query Match 100.0%; Score 31; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ADO60479
 ID ADO60479 standard; peptide; 7 AA.
 AC ADO60479;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse antibody 83-14 light chain CDR2.
 XX
 KM neuroprotective; targeted therapy; humanised antibody;
 KM human insulin receptor; HIR; heavy chain; constant region;
 KM variable region; complementarity determining region; CDR; framework;
 KM neuropharmaceutical agent; blood brain barrier; avidin-biotin linkage;
 KM mouse; antibody 83-14; Mab 83-14; light chain variable region; VL; CDR.
 XX
 OS Mus sp.
 XX
 PN US2004101904-A1.
 XX
 PD 27-MAY-2004.
 XX

RESULT 6
 ABR55336
 ID ABR55336 standard; peptide; 30 AA.
 AC ABR55336;
 XX
 DT 29-JUL-2003 (first entry)
 XX
 DE Amino acid sequence of cassette used to construct a light chain graft.
 XX
 KM Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;
 KM complementarity determining region; vascular endothelial growth factor;
 KM CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.
 XX
 OS Synthetic.
 XX

PN WO2003031475-A2.
 XX 17-APR-2003.
 XX
 XX 10-OCT-2002; 2002WO-GB004619.
 XX
 XX 10-OCT-2001; 2001GB-00024317.
 XX
 XX (CELL-) CELUTECH R & D LTD.
 PA
 PI Popplewell AG, Tickle SP, Zinkewich-Beotti K, Morrison RK;
 XX
 XX WPI; 2003-441133/41.
 DR N-PSDB; ACC70039.
 XX
 XX Novel antibody molecules having specificity for human kinase insert
 PT domain-containing receptors, useful for treating inflammation, psoriasis,
 PT rheumatoid arthritis, tumor growth and metastasis.
 XX
 XX Example; Fig 13; 57pp; English.
 PS
 XX The specification describes an antibody molecule which has specificity
 CC for human kinase insert domain-containing receptor (KDR). The antibody
 CC comprises complementarily determining regions (CDRs) from the heavy and
 CC light chain variable domains of the murine monoclonal antibody VRI65.
 CC This antibody is specific for human KDR. The antibody of the invention
 CC blocks vascular endothelial growth factor (VEGF) binding to KDR.
 CC Antibodies of the invention are useful for treating a pathology in which
 CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
 CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
 CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
 CC growth or metastasis. The present sequence represents a cassette used to
 CC construct optimised heavy chain grafts, for production of antibody
 CC molecules of the invention
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 31; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 DB 1 ATSSLDS 7
 RESULT 7
 ADM91687
 ID ADM91687 standard; protein; 83 AA.
 XX
 AC ADM91687;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX
 XX Lawsonia intracellularis specific amino acid sequence SEQ ID NO:88.
 DE
 XX Lawsonia intracellularis; infection; antibacterial; immunotherapy;
 KM proliferative enteropathy.
 XX
 XX Lawsonia intracellularis.
 OS
 XX
 PN WO2004033631-A2.
 PD
 PD 22-APR-2004.
 XX
 PF 01-OCT-2003; 2003WO-US031318.
 XX
 PR 04-OCT-2002; 2002US-0416395P.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Kapur V, Gebhart CJ;
 XX

DR WPI; 2004-340902/31.
 DR N-PSDB; ADM91625.
 XX
 XX New nucleic acid that generates an amplification product from L.
 PT intracellularis nucleic acid using an appropriate second nucleic acid
 PT molecule, useful for treating and preventing L. intracellularis
 PT infection.
 XX
 XX Disclosure; SEQ ID NO 88; 87pp; English.
 PS
 XX
 XX The present invention describes an isolated nucleic acid comprising a
 CC nucleic acid molecule of at least 10 nucleotides in length having at
 CC least 75% identity to SEQ ID NO:8741 (ADM91733), where any of the
 CC molecule that is 10-29 nucleotides in length, under standard
 CC amplification conditions, generates an amplification product from
 CC Lawsonia intracellularis nucleic acid using an appropriate second nucleic
 CC acid molecule. Also described: (1) a vector comprising the nucleic acid;
 CC (2) a host cell comprising the vector; (3) an isolated polypeptide
 CC encoded by the nucleic acid; (4) an article of manufacture comprising the
 CC polypeptide; (5) an antibody having specific binding affinity for the
 CC polypeptide; (6) a method for detecting the presence or absence of L.
 CC intracellularis in a biological sample; (7) a method of preventing
 CC infection by L. intracellularis in an animal; (8) a composition
 CC comprising a first oligonucleotide primer and a second oligonucleotide
 CC primer, where the first and second primers are each 10 to 50 nucleotides
 CC in length, and where in the presence of L. intracellularis nucleic acid,
 CC generate an amplification product under standard amplification
 CC conditions, but do not generate an amplification product in the presence
 CC of nucleic acid from an organism other than L. intracellularis; and (9)
 CC an article of manufacture comprising the composition. The nucleic acid
 CC sequence has antibacterial activity, and can be used in immunotherapy.
 CC The nucleic acid and polypeptides are useful for treating and preventing
 CC L. intracellularis infection e.g. proliferative enteropathy. The present
 CC sequence represents an L. intracellularis specific amino acid sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 83 AA;
 Query Match 100.0%; Score 31; DB 8; Length 83;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 DB 6 ATSSLDS 12
 RESULT 8
 AAR80078
 ID AAR80078 standard; protein; 90 AA.
 XX
 AC AAR80078;
 XX
 XX 22-MAY-1996 (first entry)
 DT
 XX
 XX Mouse derived light chain RT3 phage antibody pattern A.
 DE
 XX
 XX Light chain; RT3; murine, catalytic antibody; bacteriophage; pattern A.
 KM
 XX
 XX Mus musculus.
 OS
 XX
 XX
 XX Key
 FH
 FH Region
 FT 1..15
 FT /note= "framework region 1"
 FT 16..26
 FT /note= "complementarity determining region 1"
 FT 27..40
 FT /note= "framework region 2"
 FT 41..47
 FT /note= "complementarity determining region 2"
 FT 48..78
 FT /note= "framework region 3"
 FT 79..88
 FT Region

PA (KENT/) KENTEN J H.
PA (SMIT/) SMITH R.
PA (FITZ/) FITZGERALD K.
PA (WILL/) WILLIAMS R O.
XX
PI Fitzgerald K, Daraley MJ, Williams RO, Smith R, Martin MT;
PI Kenten JH, Chiswell D, Mc Cafferty J, Tiltmas RC;
XX
DR WPI; 1999-105036/09.
DR N-PSDB; AAX00875.
XX
PT Production of catalytic antibodies displayed on bacteriophages -
PT comprises generating a gene library of antibody-derived domains inserting
PT coding into a phage expression vector and isolating the catalytic
PT antibodies.
XX
XX Example 4; Fig 9A-F; 117pp; English.
XX
PS The invention relates to methods for producing catalytic antibodies
CC displayed on a phage. The method comprises: (a) generating a gene library
CC of antibody-derived domains; (b) inserting coding for the domains into a
CC phage expression vector; and (c) isolating the catalytic antibodies. The
CC phage expression vector incorporates a histidine peptide in tandem with a
CC myc peptide. The catalytic antibodies can be isolated by preparing an
CC antigen; optionally immunising an animal with the antigen; generating a
CC library of VH and VL domains from the immunised animal; cloning the VH
CC and VL domains into a phage expression vector to generate phage display
CC antibodies; selecting phage display antibodies which bind specifically to
CC the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a produg. The
CC present sequence represents a generic sequence of light chain pattern A
CC from mouse derived R13 phage antibodies
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 31; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 42 ATSSIDS 48

RESULT 11
AAW70954
ID AAW70954 standard; protein; 95 AA.
XX
AC AAW70954;
XX
DT 14-OCT-1998 (first entry)
XX
DE Light chain of monoclonal antibody RS-255.
XX
XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KM respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KM viral infection; inhibit; fusion; protection; transcription;
KM antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Mus sp.
XX
PN FR2758331-A1.
XX
PD 17-JUL-1998.
XX
PF 14-JAN-1997; 97FR-00000300.
XX
PR 14-JAN-1997; 97FR-00000300.
XX
PA (UYBO-) UNIV BOURGOGNE.

XX
DR WPI; 1998-390320/34.
XX
XX New peptide(s) recognising viral epitope with tropism to mucosa - useful
PT for, e.g. diagnosing, preventing and treating viral infection(s).
XX
PS Disclosure; Fig 2; 51pp; French.
XX
XX The present sequence represents the light chain of monoclonal antibody RS
CC -255, which is directed against the respiratory syncytial virus (RSV).
CC The specification describes peptides which recognise, by antigen-antibody
CC type reactions, at least 1 epitope of a pathogenic virus having tropism
CC for the mucosa. AAW70905-16 and AAW70923-46 are analogous to CDR regions
CC of monoclonal antibodies specific for RSV. AAW70917-28 are analogous to
CC CDR regions of monoclonal antibodies specific for site III or IV of the
CC VP6 protein of rota virus (RV). The peptides can neutralise viral
CC infections and may also inhibit fusion between infected and uninfected
CC cells or cells and viruses. They provide passive or active protection
CC and/or inhibit transcription of the virus, so are useful as antiviral
CC agents or for prophylaxis, in human or veterinary medicine. The peptides
CC can be labelled and used to diagnose infection or contamination by the
CC virus. The peptides are particularly directed against RSV or RS but may
CC also be used against papilloma, adeno, entero, polio, influenza or immune
CC deficiency viruses
XX
SQ Sequence 95 AA;

Query Match 100.0%; Score 31; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 37 ATSSIDS 43

RESULT 12
ABP33764
ID ABP33764 standard; protein; 97 AA.
XX
AC ABP33764;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human transport protein-like ORF2737 protein, SEQ ID NO:5474.
XX
XX Human; ORF; open reading frame; ORF; drug screening; diagnosis;
KM disease monitoring; cytokine; cell proliferation; cell differentiation;
KM immune modulation; haematopoiesis regulation; tissue growth;
KM angiogenesis; activin; inhibin; chemotactic; chemokine; haemostatic;
KM thrombolytic; tumour inhibition; bodily characteristic; fertility;
KM behaviour; cancer; proliferative disorder; neurological disorder;
KM cardiovascular disease; immune system disorder; organ transplantation;
KM tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KM hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KM vasotropic; antipsoriatic; antidiabetic; cytostatic; noctropic;
KM neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KM cardiac; hypotensive; antichyroid; antiinflammatory; immunomodulator;
KM dermatological; analgesic; virucide; antibacterial; fungicide.
XX
OS Homo sapiens.
XX
PN WO200190366-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US017076.
XX
PR 24-MAY-2000; 2000US-0206690P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Leach MD, Shinkets RA;


```

XX  WPI: 2002-106200/14.
XX  N-PSDB; ABN77790.
DR  Novel human polypeptides and polynucleotides useful for diagnosing,
XX  preventing and treating cardiovascular disease, neurodegenerative,
PT  hyperproliferative disorders and disorders related to organ
PT  transplantation.
XX  Claim 10; Page 1619-1620; 2508pp; English.
XX
XX  Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC  designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC  ABN79587 represent cDNAs encoding them. The invention also encompasses
CC  polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC  referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC  the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC  polynucleotides, the recombinant production of ORFX proteins, antibodies
CC  specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC  polypeptides, methods of screening for modulators of ORFX expression or
CC  activity, and methods of screening individuals for a predisposition to an
CC  ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC  range of biological activities, such as cytokine, cell proliferation,
CC  cell differentiation, immune modulation, haematopoiesis regulation,
CC  tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC  chemokinetic activity, haemostatic activity, tumour inhibition activity,
CC  receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC  and antiinfective activity, and may also be involved in the determination
CC  of bodily characteristics, fertility and behaviour. ORFX proteins,
CC  nucleic acids and antibodies may be used in the treatment of cancers,
CC  other proliferative disorders such as psoriasis and benign tumours,
CC  neurological disorders such as epilepsy and Alzheimer's disease,
CC  cardiovascular diseases, immune system disorders, disorders related to
CC  organ transplantation, disorders of tissue growth and regeneration,
CC  diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC  storage disease, and infectious diseases caused by viral, bacterial,
CC  fungal and other pathogens. ORFX nucleic acids may also be used as a
CC  source of primers and probes, in the detection of ORFX genomic sequences
CC  or transcripts, in the identification and cloning of homologous
CC  sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC  nucleic acids may additionally be used to produce transgenic animals
CC  which may be useful for studying the function and/or activity of ORFX
CC  protein, and in drug screening. The ORFX proteins may also be used as
CC  immunogens to generate specific antibodies, which are useful in the
CC  diagnosis, treatment and monitoring of ORFX-associated diseases
CC
XX  Sequence 97 AA:
SQ

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```

Query Match      100.0%; Score 31; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  1 ATSSLDS 7
    |||||
DB  52 ATSSLDS 58

```

```

RESULT 13
ADM78077
ID  ADM78077 standard; protein; 99 AA.
XX
AC  ADM78077;
XX
DT  01-JUL-2004 (first entry)
XX
XX  Human 5A3-86 antibody variable light chain region, SEQ ID NO 40.
DE
XX  monoclonal antibody; adenylate kinase isozyme 3;
KW  complementarity determining region; CDR; heart disease; marker AK3;
XX  biochemical; human; variable; light chain.
XX
OS  Homo sapiens.
XX

```

```

PN  WO2004029094-A1.
XX
XX  08-APR-2004.
PD
XX
XX  27-SEP-2003; 2003WO-KR001979.
PF
XX
XX  28-SEP-2002; 2002KR-00059211.
PR
XX
XX  (KIMH/) KIM H.
PA
XX
XX  Kim H;
PI
XX
XX  WPI: 2004-316088/29.
DR  N-PSDB; ADM78076.
XX
XX  New monoclonal antibody specific to human mitochondrial adenylate kinase
PT  isozyme 3, useful for preparing a composition for detecting a heart
PT  disease marker AK3.
XX
XX  Example 5; SEQ ID NO 40; 126pp; English.
PS
XX
XX  The invention relates to a novel monoclonal antibody specific to
CC  adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity
CC  determining regions (CDRs) of a sequence having 6-18 amino acids. The
CC  invention further relates to: a composition comprising the monoclonal
CC  antibody for detecting a heart disease marker AK3; a kit comprising the
CC  monoclonal antibody for the diagnosis of heart disease; and a method of
CC  detecting a heart disease marker AK3. The monoclonal antibody is useful
CC  for preparing a composition for detecting a heart disease marker AK3. The
CC  monoclonal antibody reduces false positive results of the conventional
CC  biochemical markers. This sequence represents a human variable light
CC  chain region protein of the invention.
XX

```

```

SQ Sequence 99 AA:

```

```

Query Match      100.0%; Score 31; DB 8; Length 99;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  1 ATSSLDS 7
    |||||
DB  41 ATSSLDS 47

```

```

RESULT 14
AAW27121
ID  AAW27121 standard; protein; 107 AA.
XX
XX  AAW27121;
AC
XX
XX  25-MAR-2003 (revised)
DT  04-JAN-1998 (first entry)
DT
XX
XX

```

```

DE  Murine antibody light chain variable region consensus.

```

```

KW  Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
XX  human milk fat globule; HMEG; tumour; breast cancer; vaccine.
XX

```

```

OS  Mus musculus.
XX

```

```

FH  Location/Qualifiers

```

```

FT  Region

```

```

FT  /label= CDR1
FT  /note= "complementarity determining region 1"

```

```

FT  Region

```

```

FT  /label= CDR2
FT  /note= "complementarity determining region 2"

```

```

FT  Region

```

```

FT  /label= CDR3
FT  /note= "complementarity determining region 3"

```

```

XX  WO9722699-A2.
XX

```

PD 26-JUN-1997.
XX
PF 19-DEC-1996; 96WO-US020757.
XX
PR 20-DEC-1995; 95US-00575762.
PR 26-JAN-1996; 96US-00591965.
PR 13-DEC-1996; 96US-00766350.
XX
PA (KENT) UNIV KENTUCKY.
PI Charterjee M, Foon KA, Charterjee SK.
DR WPI; 1997-341690/31.
XX
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against
PT human milk fat globule disease associated tumours, especially breast
PT cancer.
PS Example 2; Fig 26C; 130pp; English.
XX
XX This polypeptide sequence comprises a consensus sequence of murine light
CC chain variable regions (VL) selected on the basis of identity to the VL
CC region (see W27119) of monoclonal anti-idiotypic antibody 11D10. The
CC sequences were obtained from a GenBank database search. A VH consensus
CC (W27122) was also produced. 11D10 has at least 18 departures from the
CC consensus sequences (7 in the light chain and 11 in the heavy chain). 8
CC occur within CDRs and 10 outside CDRs. 11D10 polypeptides and
CC polynucleotides can be used in vaccines and pharmaceutical compositions
CC for the treatment of human milk fat globule-associated diseases such as
CC breast cancer. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 15

AA90824
ID AAY90824 standard; protein; 107 AA.

XX
AC AAY90824;

XX
DT 29-AUG-2000 (first entry)

XX
DE 520C9 hybridoma VL domain SEQ ID NO:26.

XX
KW Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
KW specific binding assay; affinity purification; drug targeting;
KW toxin targeting; imaging; genetic; therapeutic.

XX
OS Homo sapiens.

XX
PN US6054561-A.

XX
PD 25-APR-2000.

XX
PF 07-JUN-1995; 95US-00483749.

XX
PR 08-FEB-1984; 84US-00577976.

PR 11-JAN-1985; 85US-00690750.

PR 21-MAR-1986; 86US-00842476.

PR 08-MAY-1988; 88US-00190778.

PR 11-AUG-1994; 94US-00288981.
XX
PA (CHIR) CHIRON CORP.
XX

PI Ring DB;
XX
XX WPI; 2000-338508/29.
DR N-PsDB; AAA38908.
XX
PT Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer.

XX
PS Disclosure; Fig 13; 57pp; English.

XX
XX The present invention describes a monoclonal antibody (Mab) (I) that
CC binds to a human breast cancer antigen that is also bound by Mab 454C11
CC and 520C9 (produced by hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The
CC present sequence represents a VL domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention

XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
Db 50 ATSSIDS 56

Search completed: April 4, 2005, 15:47:17
Job time : 15.9776 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 10.3323 Seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_183_189

Perfect score: 31
Sequence: 1 ATSSIDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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| 1: | /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.* |
| 2: | /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.* |
| 3: | /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.* |
| 4: | /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.* |
| 5: | /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.* |
| 6: | /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.* |
| 7: | /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.* |
| 8: | /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.* |
| 9: | /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.* |
| 10: | /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.* |
| 11: | /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.* |
| 12: | /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.* |
| 13: | /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.* |
| 14: | /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.* |
| 15: | /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.* |
| 16: | /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.* |
| 17: | /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.* |
| 18: | /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.* |
| 19: | /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.* |
| 20: | /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|---------------------|
| 1 | 31 | 100.0 | 7 | US-09-924-099-4 |
| 2 | 31 | 100.0 | 7 | US-10-307-276B-40 |
| 3 | 31 | 100.0 | 97 | US-09-864-408A-5474 |
| 4 | 31 | 100.0 | 108 | US-09-924-099-1 |
| 5 | 31 | 100.0 | 108 | US-10-010-729-45 |
| 6 | 31 | 100.0 | 108 | US-10-307-276B-4 |
| 7 | 31 | 100.0 | 108 | US-10-307-276B-6 |
| 8 | 31 | 100.0 | 108 | US-10-803-622-267 |
| 9 | 31 | 100.0 | 108 | US-10-803-653-267 |
| 10 | 31 | 100.0 | 109 | US-09-943-906-74 |
| 11 | 31 | 100.0 | 109 | US-10-435-602-74 |
| 12 | 31 | 100.0 | 112 | US-10-355-780-1 |
| 13 | 31 | 100.0 | 130 | US-08-779-784-35 |

| | | | | | |
|----|----|-------|-----|---------------------|-------------------|
| 14 | 31 | 100.0 | 130 | US-10-010-729-71 | Sequence 71, Appl |
| 15 | 31 | 100.0 | 144 | US-10-642-120-4 | Sequence 4, Appl |
| 16 | 31 | 100.0 | 144 | US-10-642-060-4 | Sequence 4, Appl |
| 17 | 31 | 100.0 | 144 | US-10-642-122-4 | Sequence 4, Appl |
| 18 | 31 | 100.0 | 144 | US-10-642-124-4 | Sequence 4, Appl |
| 19 | 31 | 100.0 | 144 | US-10-621-269-4 | Sequence 4, Appl |
| 20 | 31 | 100.0 | 144 | US-10-620-850-4 | Sequence 4, Appl |
| 21 | 31 | 100.0 | 144 | US-10-642-116-4 | Sequence 4, Appl |
| 22 | 31 | 100.0 | 144 | US-10-642-100-4 | Sequence 4, Appl |
| 23 | 31 | 100.0 | 144 | US-10-642-058-4 | Sequence 4, Appl |
| 24 | 31 | 100.0 | 147 | US-10-642-121-4 | Sequence 4, Appl |
| 25 | 31 | 100.0 | 147 | US-10-106-698-6340 | Sequence 6340, Ap |
| 26 | 31 | 100.0 | 234 | US-10-369-493-9621 | Sequence 9621, Ap |
| 27 | 31 | 100.0 | 236 | US-10-879-994-6 | Sequence 6, Appl |
| 28 | 31 | 100.0 | 237 | US-09-924-099-9 | Sequence 9, Appl |
| 29 | 31 | 100.0 | 243 | US-09-924-099-10 | Sequence 10, Appl |
| 30 | 31 | 100.0 | 243 | US-09-887-853-6 | Sequence 6, Appl |
| 31 | 31 | 100.0 | 243 | US-10-683-547-6 | Sequence 6, Appl |
| 32 | 31 | 100.0 | 252 | US-10-239-656-55 | Sequence 55, Appl |
| 33 | 31 | 100.0 | 257 | US-10-239-656-67 | Sequence 67, Appl |
| 34 | 31 | 100.0 | 267 | US-09-766-543-10 | Sequence 10, Appl |
| 35 | 31 | 100.0 | 276 | US-09-766-543-12 | Sequence 12, Appl |
| 36 | 31 | 100.0 | 476 | US-10-369-493-19774 | Sequence 19774, A |
| 37 | 31 | 100.0 | 483 | US-10-369-493-10092 | Sequence 10092, A |
| 38 | 31 | 100.0 | 499 | US-10-239-656-73 | Sequence 73, Appl |
| 39 | 31 | 100.0 | 510 | US-10-369-493-19611 | Sequence 19611, A |
| 40 | 31 | 100.0 | 566 | US-10-369-493-4440 | Sequence 4440, Ap |
| 41 | 31 | 100.0 | 567 | US-10-369-493-7199 | Sequence 7199, Ap |
| 42 | 31 | 100.0 | 574 | US-10-369-493-14607 | Sequence 14607, A |
| 43 | 31 | 100.0 | 575 | US-10-369-493-14397 | Sequence 14397, A |
| 44 | 31 | 100.0 | 577 | US-10-369-493-10270 | Sequence 10270, A |
| 45 | 31 | 100.0 | 583 | US-10-369-493-11412 | Sequence 11412, A |

ALIGNMENTS

RESULT 1
US-09-924-099-4
; Sequence 4, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924, 099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338, 511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289, 044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365, 023/98
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-4

Query Match 100.0%; Score 31; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
| | | | |
DB 1 ATSSIDS 7

RESULT 2

US-10-307-276B-40
; Sequence 40, Application US/10307276B
; Publication No. US20040101904A1
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/307,276B
; FILING DATE: 27-Nov-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO:40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40
US-10-307-276B-40

Query Match 100.0%; Score 31; DB 16; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 1 ATSSIDS 7

RESULT 3
US-09-864-408A-5474

; Sequence 5474, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5474
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5474

Query Match 100.0%; Score 31; DB 11; Length 97;

Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 52 ATSSIDS 58

RESULT 4

US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takamori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match 100.0%; Score 31; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
Db 50 ATSSIDS 56

RESULT 5

US-10-010-729-45
; Sequence 45, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 108

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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-45
Query Match      100.0%; Score 31; DB 14; Length 103;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db      50 ATSSIDS 56

RESULT 6
US-10-307-276B-4
; Sequence 4, Application US/10307276B
; Publication No. US20040101904A1
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
;
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/307,276B
; FILING DATE: 27-Nov-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-307-276B-4

Query Match      100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db      50 ATSSIDS 56

RESULT 7
US-10-307-276B-6
; Sequence 6, Application US/10307276B
; Publication No. US20040101904A1
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
```

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; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/307,276B
; FILING DATE: 27-Nov-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-10-307-276B-6

Query Match      100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSIDS 7
        |||||
Db      50 ATSSIDS 56

RESULT 8
US-10-803-622-267
; Sequence 267, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kaeper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-0003
; CURRENT APPLICATION NUMBER: US/10/803,622
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
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PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patentin version 3.1
SEQ ID NO 267
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain from clone M1F
US-10-803-622-267

Query Match 100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 50 ATSSLDS 56

RESULT 9
US-10-803-653-267
Sequence 267, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893

PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patentin version 3.1
SEQ ID NO 267
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain from clone M1F
US-10-803-653-267

Query Match 100.0%; Score 31; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 50 ATSSLDS 56

RESULT 10
US-09-943-906-74
Sequence 74, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PRP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 100.0%; Score 31; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 50 ATSSLDS 56

Db 50 ATSSIDS 56

RESULT 11

US-10-435-602-74
; Sequence 74, Application US/10435602
; Publication No. US2003022833A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: Antibodies Specific for Native PrPsc
; FILE REFERENCE: UCAL059CON3
; CURRENT APPLICATION NUMBER: US/10/435,602
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 09/943,906
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/550,374
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 09/036,579
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 08/713,939
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: 08/528,104
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-10-435-602-74

Query Match 100.0%; Score 31; DB 15; Length 10%;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7

Db 50 ATSSIDS 56

RESULT 12

US-10-355-780-1
; Sequence 1, Application US/10355780
; Publication No. US2003014322A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley
; APPLICANT: Safar, Jiri
; APPLICANT: Williamson, Anthony
; APPLICANT: Burton, Dennis
; TITLE OF INVENTION: Antibodies Specific for Ungulate PrP
; FILE REFERENCE: UCAL-194
; CURRENT APPLICATION NUMBER: US/10/355,780
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 08/09/627,2188
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide
US-10-355-780-1

Query Match 100.0%; Score 31; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7

Db 50 ATSSIDS 56

RESULT 13

US-08-779-784-35
; Sequence 35, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Aaskura, Kunitiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match 100.0%; Score 31; DB 8; Length 130;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7

Db 72 ATSSIDS 78

RESULT 14

US-10-010-729-71
; Sequence 71, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.

APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 130
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-71

Query Match 100.0%; Score 31; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|||||
Db 72 ATSSIDS 78

RESULT 15
US-10-642-120-4
Sequence 4, Application US/10642120
Publication No. US20040131610A1
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Soares, M. Melina
TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
TITLE OF INVENTION: Aminoalcohols
FILE REFERENCE: 4001.002900
CURRENT APPLICATION NUMBER: US/10/642,120
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 10/621,269
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,263
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 144
TYPE: PRT
ORGANISM: Mus musculus
US-10-642-120-4

Query Match 100.0%; Score 31; DB 16; Length 144;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|||||
Db 72 ATSSIDS 78

Search completed: April 4, 2005, 16:42:45
Job time : 11.3323 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 2.52716 seconds
(without alignments)

266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_183_189

Perfect score: 31

Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 31 | 100.0 | 88 | 2 | PL0261 |
| 2 | 31 | 100.0 | 106 | 2 | PL0260 |
| 3 | 31 | 100.0 | 106 | 2 | PL0259 |
| 4 | 31 | 100.0 | 130 | 1 | KVMSM4 |
| 5 | 31 | 100.0 | 131 | 2 | E97737 |
| 6 | 31 | 100.0 | 320 | 2 | A13469 |
| 7 | 31 | 100.0 | 548 | 2 | F71732 |
| 8 | 31 | 100.0 | 555 | 2 | S63137 |
| 9 | 31 | 100.0 | 589 | 2 | D70031 |
| 10 | 31 | 100.0 | 589 | 2 | F97735 |
| 11 | 31 | 100.0 | 600 | 2 | AD3138 |
| 12 | 31 | 100.0 | 600 | 2 | H98149 |
| 13 | 31 | 100.0 | 604 | 2 | H95974 |
| 14 | 31 | 100.0 | 604 | 2 | S60182 |
| 15 | 31 | 100.0 | 1025 | 2 | T18376 |
| 16 | 31 | 100.0 | 1419 | 1 | DVZOP |
| 17 | 28 | 90.3 | 327 | 2 | F71800 |
| 18 | 28 | 90.3 | 327 | 2 | H64716 |
| 19 | 28 | 90.3 | 428 | 2 | T43532 |
| 20 | 28 | 90.3 | 534 | 2 | S77239 |
| 21 | 28 | 90.3 | 546 | 2 | AG1886 |
| 22 | 28 | 90.3 | 571 | 2 | S58356 |
| 23 | 28 | 90.3 | 575 | 2 | AH1417 |
| 24 | 28 | 90.3 | 575 | 2 | AB1793 |
| 25 | 28 | 90.3 | 578 | 2 | AB3739 |
| 26 | 28 | 90.3 | 584 | 2 | G86713 |
| 27 | 28 | 90.3 | 587 | 2 | AD3122 |
| 28 | 28 | 90.3 | 587 | 2 | C98165 |
| 29 | 28 | 90.3 | 588 | 2 | A75282 |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 30 | 28 | 90.3 | 607 | 2 | A35391 | heA protein - Ana |
| 31 | 28 | 90.3 | 607 | 2 | AD2160 | heterocyst differe |
| 32 | 28 | 90.3 | 609 | 2 | G71731 | mitochondrial tran |
| 33 | 28 | 90.3 | 610 | 2 | H83243 | probable ATP-bindi |
| 34 | 28 | 90.3 | 611 | 2 | H82351 | probable hemolysin |
| 35 | 28 | 90.3 | 614 | 2 | A64180 | probable ATP-bindi |
| 36 | 28 | 90.3 | 616 | 2 | A12851 | hypothetical prote |
| 37 | 28 | 90.3 | 618 | 2 | B81796 | probable ABC trans |
| 38 | 28 | 90.3 | 618 | 2 | AB1218 | ABC transporter, A |
| 39 | 28 | 90.3 | 619 | 2 | F82391 | ABC transporter, A |
| 40 | 28 | 90.3 | 622 | 2 | AB3311 | ABC transporter AT |
| 41 | 28 | 90.3 | 626 | 2 | A13310 | ABC transporter AT |
| 42 | 28 | 90.3 | 627 | 2 | AH2851 | hypothetical prote |
| 43 | 28 | 90.3 | 633 | 2 | T27215 | hypothetical prote |
| 44 | 28 | 90.3 | 633 | 2 | G97628 | ATP-binding protei |
| 45 | 28 | 90.3 | 634 | 2 | T48418 | ABC transporter-11 |

ALIGNMENTS

RESULT 1
PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C:Accession: PL0261
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0261
A:Molecule type: mRNA
A:Residues: 1-88 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Region: framework 1
F:6-16/Region: complementarity-determining 1
F:17-31/Region: framework 2
F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 32 ATSSLDS 38

RESULT 2
PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0260
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 3

Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: P10259

R/Shlomchik, M.; Macceilli, M.; Shan, H.; Radic, M.Z.; Plesetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990

A>Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: P10231; MUID:90111618; PMID:2104919

A/Accession: P10259
A/Molecule type: mRNA
A/Residues: 1-106 <SHL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 4

Ig kappa chain precursor V region (MOPC 41) - mouse

N/Contents: Ig kappa chain precursor V region VK41
C/Species: Mus musculus (house mouse)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C/Accession: A93211; B93211; A93815; A94239; A01922; A01923

R/Seidman, J.G.; Max, E.E.; Leder, P.

Nature 280, 370-375, 1979
A>Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A/Reference number: A93211; MUID:79221900; PMID:111146

A/Accession: A93211
A/Molecule type: DNA
A/Residues: 1-130 <PC41>

A/Cross-references: UNIPROT:P01639
A/Accession: B93211

A/Molecule type: DNA
A/Residues: 1-117 <RV41>

A/Cross-references: GB:V00804; GB:J00566; NID:952127; PIDN:CAA24186.1; PID:9575660
A/Note: the sequences were determined from the differentially expressed MOPC 41 and the germ

R/Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A>Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor
A/Reference number: A93815; MUID:77148916; PMID:403522

A/Accession: A93815
A/Molecule type: protein
A/Residues: 1-33 <BUR>

A/Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R/Gray, W.R.; Dreyer, W.U.; Hood, L.

Science 155, 465-467, 1967
A>Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A/Reference number: A94239; MUID:67056897; PMID:4162931

A/Accession: A94239
A/Molecule type: protein
A/Residues: 23-49, 'B', 51-53, 'LSB', 57-58, 'ZZ', 61-62, 'BZ', 65-76, 'B', 78-108, 110-130 <GRA>

A/Experimental source: Bence Jones protein MOPC 41
C/Genetics:

A/Introns: 19/1
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into lat

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: alternative initiators; heterotrimer; immunoglobulin

F:1-22/Domain: signal sequence #status experimental <SIG1>
F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 72 ATSSLDS 78

RESULT 5

E97737
hypothetical protein RC0301 [imported] - Rickettsia conorii (strain Malish 7)

C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001
A>Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.

A/Reference number: A97700; MUID:2142074; PMID:11557893

A/Accession: E97737
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-131 <KUR>
A/Cross-references: UNIPROT:Q921W9; GB:AE006914; PIDN:AAL02839.1; PID:GL5619360; GSPDB:GT

A/Genetics:
C/Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 62 ATSSLDS 68

RESULT 6

A13469
ABC transporter ATP-binding protein BME11743 [imported] - Brucella melitensis (strain 16b

C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C/Accession: A13469
R/DelVecchio, V.G.; Kapatal, V.; Redkar, R.U.; Patra, G.; Mujer, C.; Loe, T.; Ivanova, I

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688
A/Accession: A13469
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-320 <KUR>

A/Cross-references: UNIPROT:O8YEX4; GB:AE008917; PIDD:AA152924.1; PID:gl7983771; GSPDB:C
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME11743
A/Map position: 1

Query Match 100.0%; Score 31; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 235 ATSSLDS 241

RESULT 7
ABC transporter ATP-binding protein (abcT3) RP214 - Rickettsia prowazekii
C/Species: Rickettsia prowazekii
C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 16-Aug-2004
A/Cross-references: F71732
R/Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A/Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A/Reference number: A71630; MUID:99039499; PMID:9823893
A/Accession: F71732
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-548 <AND>
A/Cross-references: UNIPROT:Q9ZDV5; GB:AJ235270; GB:AJ235269; NID:g3660572; PIDD:CAA1467
A/Experimental source: strain Madrid E
C/Genetics:
A/Gene: abcT3; RP214
C/Superfamily: ATP-binding cassette homology
C/Keywords: ATP
P.323-517/Domain: ATP-binding cassette homology <ABC>

Query Match 100.0%; Score 31; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 470 ATSSLDS 476

RESULT 8
S63137
hypothetical protein YNL182c - yeast (Saccharomyces cerevisiae)
M/Alternate names: hypothetical protein N1636
C/Species: Saccharomyces cerevisiae
C/Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
A/Accession: S63137
R/Obermayer, B.; Piravandi, E.; Rinke, M.; Domdey, H.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S63122
A/Accession: S63137
A/Molecule type: DNA
A/Residues: 1-555 <OBE>
A/Cross-references: UNIPROT:P53877; EMBL:Z71458; NID:g1302165; PID:e239555; PID:g1302166
A/Experimental source: strain S286C
C/Genetics:
A/Gene: MIPS:YNL182c
A/Cross-references: SGD:S0005126
A/Map position: 14L

Query Match 100.0%; Score 31; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 506 ATSSLDS 512

RESULT 9
D70031
ABC transporter (ATP-binding protein) homolog yvcc - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A/Accession: D70031
R/Kunec, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteric
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galazzi, A.; Gallier
iech, U.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,
akuehl, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumelein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: D70031
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-589 <KUN>
A/Cross-references: UNIPROT:O06967; GB:Z99121; GB:AL009126; NID:g2635827; PIDD:CAB15487.J
A/Experimental source: strain 168
C/Genetics:
A/Gene: yvcc
C/Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology
C/Keywords: ATP; nucleotide binding; P-loop
P.357-552/Domain: ATP-binding cassette homology <ABC>
P.374-381/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 505 ATSSLDS 511

RESULT 10
F97735
hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7)
C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
A/Accession: F97735
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rol
science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A/Reference number: A97700; MUID:21442074; PMID:11557893
A/Accession: F97735
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-589 <KUR>
A/Cross-references: UNIPROT:Q921Y4; GB:AE006914; PIDD:AA102824.1; PID:g15619343; GSPDB:GT
C/Genetics:
A/Gene: abcT3
C/Superfamily: ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
|||||
Db 511 ATSSLDS 517

RESULT 11
AD3138
Hypothetical protein exsA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:/Species: Agrobacterium tumefaciens
C:/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:/Accession: AD3138
R:/Wood, D.W.; Seubald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:/Reference number: AB25777; MUID:21608550; PMID:11743193
A:/Accession: AD3138
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-600 <KUR>
A:/Cross-references: UNIPROT:Q8U6S8; GB:AB008689; PIDN:AL45522.1; PID:G17743233; GSPDB:C
A:/Experimental source: strain C58 (Dupont)
C:/Genetics:
A:/Gene: exsA
A:/Map position: linear chromosome
C:/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
Query Match 100.0%; Score 31; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
|||||
Db 517 ATSSIDS 523
RESULT 12
H98149
ATP-binding transport protein exsA [imported] - Agrobacterium tumefaciens (strain C58, C
C:/Species: Agrobacterium tumefaciens
C:/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
C:/Accession: H98149
R:/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:/Reference number: A97359; MUID:21608551; PMID:11743194
A:/Accession: H98149
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-600 <KUR>
A:/Cross-references: UNIPROT:Q8U6S8; GB:AB007870; PIDN:AAK89722.1; PID:G15150459; GSPDB:C
C:/Genetics:
A:/Gene: AGR_L_309
A:/Map position: linear chromosome
Query Match 100.0%; Score 31; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
|||||
Db 517 ATSSIDS 523
RESULT 13
H95974
mepA-like saccharide exporting ABC transporter protein, consisting of ATP-binding and pe
C:/Species: Sinorhizobium meliloti
C:/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 16-Aug-2004
C:/Accession: H95974
R:/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N₂-fixing endo

A:/Reference number: A95842; MUID:21396508; PMID:11481431
A:/Accession: H95974
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-604 <KUR>
A:/Cross-references: UNIPROT:Q52924; GB:AL591985; PIDN:CA049464.1; PID:G15140950; GSPDB:G
R:/Experimental source: strain 1021, megaplasmid pSymB
R:/Galbert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
peta, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hepault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:/Reference number: A96039; MUID:21368234; PMID:11474104
A:/Contents: annotation
C:/Genetics:
A:/Gene: exsA; SMD20941
A:/genome: plasmid
Query Match 100.0%; Score 31; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
|||||
Db 518 ATSSIDS 524
RESULT 14
S60182
ATP-binding transport protein exsA - Rhizobium meliloti
C:/Species: Rhizobium meliloti
C:/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C:/Accession: S60182
R:/Becker, A.; Kuester, H.; Niehaus, K.; Puhler, A.
Mol. Gen. Genet. 249, 487-497, 1995
A:/Title: Extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: id
regulator of succinoglycan biosynthesis.
A:/Reference number: S60181; MUID:96133689; PMID:8544814
A:/Accession: S60182
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-604 <BEC>
A:/Cross-references: UNIPROT:Q52924; EMBL:Z50189; NID:G1143532; PIDN:CA090568.1; PID:G191
A:/Note: it is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the initiat
C:/Genetics:
A:/Gene: exsA
A:/Superfamily: ATP-binding cassette homology
C:/Keywords: ATP; nucleotide binding; P-loop
F:/571-565/Domain: ATP-binding cassette homology <ABC>
F:/388-395/Region: nucleotide-binding motif A (P-loop)
Query Match 100.0%; Score 31; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
|||||
Db 518 ATSSIDS 524
RESULT 15
T18376
multidrug resistance protein 2 - malaria parasite (Plasmodium falciparum)
C:/Species: Plasmodium falciparum
C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:/Accession: T18376
R:/Kubio, J.P.; Cowman, A.F.
Exp. Parasitol. 79, 137-147, 1994
A:/Title: Plasmodium falciparum: the pfmdr2 protein is not overexpressed in chloroquine-re
A:/Reference number: Z18924; MUID:94333528; PMID:7914495
A:/Accession: T18376

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1025 <RUB>
A:Cross-references: UNIPROT:Q25693; EMBL:U04640; NID:g439853; FID:g439854; PIDN:AAA21513
C/Genetics:
A/Gene: mdr2

Query Match 100.0%; Score 31; DB 2; Length 1025;
Best Local Similarity 100.0%; Pred. NO. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSIDS 7
|||||
Db 851 ATSSIDS 857

Search completed: April 4, 2005, 15:58:02
Job time : 3.52716 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 11.8307 seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_183_189
Perfect score: 31
Sequence: 1 ATSSIDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_aprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 31 | 100.0 | 57 | 2 Q7PB38 | Q7PB38 rickettsia |
| 2 | 31 | 100.0 | 130 | 1 KUSG_MOUSE | P01639 mus musculu |
| 3 | 31 | 100.0 | 131 | 2 Q921W9 | Q921W9 rickettsia |
| 4 | 31 | 100.0 | 320 | 2 Q8YBY4 | Q8YBY4 bruceella me |
| 5 | 31 | 100.0 | 370 | 2 Q61009 | Q61009 bacillus an |
| 6 | 31 | 100.0 | 538 | 2 Q81EL4 | Q81EL4 bacillus ce |
| 7 | 31 | 100.0 | 548 | 2 Q9ZDV5 | Q9ZDV5 rickettsia |
| 8 | 31 | 100.0 | 555 | 1 YNS2_YEAST | P53877 saccharomyc |
| 9 | 31 | 100.0 | 565 | 2 Q6KFE6 | Q6KFE6 chlamydia p |
| 10 | 31 | 100.0 | 565 | 2 Q9MBU6 | Q9MBU6 chlamydia p |
| 11 | 31 | 100.0 | 586 | 2 Q63CK1 | Q63CK1 bacillus ce |
| 12 | 31 | 100.0 | 586 | 2 Q739U8 | Q739U8 bacillus ce |
| 13 | 31 | 100.0 | 586 | 2 Q6HK05 | Q6HK05 bacillus th |
| 14 | 31 | 100.0 | 589 | 2 Q7PB25 | Q7PB25 rickettsia |
| 15 | 31 | 100.0 | 589 | 2 Q06967 | Q06967 bacillus su |
| 16 | 31 | 100.0 | 589 | 2 Q921Y4 | Q921Y4 rickettsia |
| 17 | 31 | 100.0 | 589 | 2 Q68XP5 | Q68XP5 rickettsia |
| 18 | 31 | 100.0 | 596 | 2 Q9L7X7 | Q9L7X7 bruceella ab |
| 19 | 31 | 100.0 | 596 | 2 Q8ERT1 | Q8ERT1 shewanella |
| 20 | 31 | 100.0 | 600 | 2 Q7NBB3 | Q7NBB3 mycoplasma |
| 21 | 31 | 100.0 | 600 | 2 Q8U6S8 | Q8U6S8 agrobacteri |
| 22 | 31 | 100.0 | 601 | 2 Q98LY9 | Q98LY9 rhizobium l |
| 23 | 31 | 100.0 | 602 | 2 Q82S99 | Q82S99 nitrosomona |
| 24 | 31 | 100.0 | 604 | 2 Q6WZG9 | Q6WZG9 rhizobium s |
| 25 | 31 | 100.0 | 604 | 2 Q52924 | Q52924 rhizobium m |
| 26 | 31 | 100.0 | 605 | 2 Q72QD0 | Q72QD0 leptospira |
| 27 | 31 | 100.0 | 605 | 2 Q8F5R7 | Q8F5R7 leptospira |
| 28 | 31 | 100.0 | 606 | 2 Q7KVA9 | Q7KVA9 drosophila |
| 29 | 31 | 100.0 | 610 | 2 Q7VZM6 | Q7VZM6 drosophila |
| 30 | 31 | 100.0 | 616 | 2 Q7W8H5 | Q7W8H5 bordetella |
| 31 | 31 | 100.0 | 616 | 2 Q7WM37 | Q7WM37 bordetella |

| | | | | | |
|----|----|-------|-----|--------------|--------------------|
| 32 | 31 | 100.0 | 625 | 2 Q89FS9 | Q89FS9 bradyrhizob |
| 33 | 31 | 100.0 | 626 | 2 Q6CS09 | Q6CS09 oikopleura |
| 34 | 31 | 100.0 | 631 | 2 Q98AT0 | Q98AT0 rhizobium 1 |
| 35 | 31 | 100.0 | 643 | 2 Q8KJ66 | Q8KJ66 rhizobium 1 |
| 36 | 31 | 100.0 | 669 | 2 Q62E22 | Q62E22 burkholderi |
| 37 | 31 | 100.0 | 669 | 2 Q63J56 | Q63J56 burkholderi |
| 38 | 31 | 100.0 | 694 | 1 ABC7_MOUSE | 061102 mus musculu |
| 39 | 31 | 100.0 | 709 | 2 Q7KVB1 | Q7KVB1 drosophila |
| 40 | 31 | 100.0 | 715 | 2 Q8KRA4 | Q8KRA4 rhizobium e |
| 41 | 31 | 100.0 | 743 | 1 Q9W0C5 | Q9W0C5 drosophila |
| 42 | 31 | 100.0 | 752 | 1 ABC7_HUMAN | Q75027 homo sapien |
| 43 | 31 | 100.0 | 752 | 1 Q704E8 | Q704E8 rattus norv |
| 44 | 31 | 100.0 | 888 | 2 Q7RBT4 | Q7RBT4 plasmodium |
| 45 | 31 | 100.0 | 947 | 2 Q08667 | Q08667 plasmodium |

ALIGNMENTS

RESULT 1
Q7PB38 PRELIMINARY; PRT; 57 AA.
ID Q7PB38;
AC Q7PB38;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN Name=rsib_0rf.406;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereemeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABW01000001; EAA25646.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Prodom; PD000006; ABC transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW ATP-binding
SQ SEQUENCE 57 AA; 6232 MW; 4FA4E36794DB92B8 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 48 ATSSIDS 54

RESULT 2
KVSQ_MOUSE
ID KVSQ_MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.E., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation.";
RL Nature 280:370-375(1979).
RN
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Buretein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda-delta-type and kappa-type light
RT chains";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.U., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse kappa
RT chains";
RL Science 155:465-467(1967).
CC -1- MISCELLANEOUS: This precursor was synthesized in a cell-free
CC system directed by mRNA isolated from myeloma polyomes.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSSP; A93211; KVM5M4.
DR HSSP; P01594; LUV5.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 130 Ig kappa chain V-V region MOPC 41.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DOMAIN 45 110 By similarity.
FT DISULFID 1 2 Missing (in 25% of the molecules).
FT NON TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; SEF0FE71D5F1BEC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 72 ATSSIDS 78

RESULT 3
Q921W9 PRELIMINARY; PRT; 131 AA.
AC Q921W9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN OrderedLocNames=RC0301;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;

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RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sameon D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE008596; AA02839.1; -.
DR PIR; E97737; E97737.
DR HSSP; P08716; LMT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 131 AA; 14753 MW; C848BCA612872D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
DB 62 ATSSIDS 68

RESULT 4
Q8YEY4 PRELIMINARY; PRT; 320 AA.
AC Q8YEY4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC TRANSPORTER ATP-BINDING PROTEIN.
GN OrderedLocNames=BME11743;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756588; DOI=10.1073/pnas.221575398;
RX Delvecchio V.G., Kapatal V., Redkar R.U., Patia G., Mujar C., Los T.,
RX Ivanova N., Anderson I., Bhatlacharya A., Lykdis A., Reznik G.,
RX Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman B.,
RX Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE009607; AA052924.1; -.
DR PIR; A13469; A13469.
DR HSSP; Q9KQW9; IPR4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 320 AA; 35768 MW; 95DBAB38430A2C01 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 50;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
    |||||
Db 235 ATSSIDS 241

RESULT 5
061009 PRELIMINARY; PRT; 370 AA.
AC 061009;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE ABC transporter.
GN OrderedlocusNames=BA51815;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1392;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Stearne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gina P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017225; AAT54130.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding.
SQ
SEQUENCE 370 AA; 40954 MW; 9C6683290C2C7EC3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
    |||||
Db 290 ATSSIDS 296

RESULT 6
081E14 PRELIMINARY; PRT; 538 AA.
AC 081E14;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease
DE protein.
GN OrderedlocusNames=BC1955;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=226900;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

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RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Malinas T.,
RA Grechkin Y., Busch G., Haselkorn R., Fontein M., Ehrlich S.D.,
RA Overbeek R., Kyprides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017004; AAP08926.1; -.
DR HSSP; Q9CHL8; 1MV5.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ
SEQUENCE 538 AA; 59151 MW; B70E78C62BEAC132 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
    |||||
Db 458 ATSSIDS 464

RESULT 7
092DV5 PRELIMINARY; PRT; 548 AA.
AC 092DV5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ABC TRANSPORTER ATP-BINDING PROTEIN (AbcT3).
GN OrderedlocusNames=RP214;
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxId=782;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichelitz-Ponten T., Almark U.C.M., Podowski R.M., Neeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AJ235270; CAA14677.1; -.
DR PIR; F71732; F71732.
DR HSSP; P08716; 1MT0.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.

```

DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00929; ABC_TM1F; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 DR ATP-binding; Complete proteome.
 SQ SEQUENCE 548 AA; 62589 MW; B4ED4E7F9D53EDC9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 470 ATSSLDS 476

RESULT 8
 ID YNS2_YEAST STANDARD; PRT; 555 AA.
 AC P53877;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypothetical 61.8 kDa TYP-Asp repeats containing protein in NPRI-RP53
 GN Intergenic region.
 OS OrderedLocustNames=YNL82C; ORFNames=N1636;
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M., Domdey H.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 WD repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; Z71458; CAA96075.1; -.
 DR PIR; S63137; S63137.
 DR IntAct; P53877; -.
 DR GeneOnline; 143188; -.
 DR SGD; S00005126; IPI3.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR001680; WD40.
 DR InterPro; IPR011045; WD40_like.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
 DR PROSITE; PS50082; WD_REPEATS_2; 1.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KM Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 90 133 WD 1.
 FT REPEAT 137 176 WD 2.
 FT REPEAT 187 234 WD 3.
 FT REPEAT 342 383 WD 4.
 SQ SEQUENCE 555 AA; 61773 MW; 8EED654DF9405A6 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 555;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

Db 506 ATSSLDS 512

RESULT 9
 ID Q6KF06 PRELIMINARY; PRT; 565 AA.
 AC Q6KF06;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Structural protein.
 OS Chlamydia phage 3.
 OC Viruses; ssDNA viruses; Microviridae; Chlamydia microvirus.
 OX NCBI_TaxID=225067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Garner S.A., Everson J.S., Lambden P.R., Fane B.A., Clarke I.N.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ550635; CAD79477.1; -.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR003514; Capsid_F.
 DR Pfam; PF02305; Phage_F; 1.
 SQ SEQUENCE 565 AA; 63629 MW; E8DEBAE70FA91DFE CRC64;

Query Match 100.0%; Score 31; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 497 ATSSLDS 503

RESULT 10
 ID Q9MBU6 PRELIMINARY; PRT; 565 AA.
 AC Q9MBU6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Structural protein.
 GN Name=VP1;
 OS Chlamydia phage 2.
 OC Viruses; ssDNA viruses; Microviridae; Chlamydia microvirus.
 OX NCBI_TaxID=105154;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193783; PubMed=10729119;
 RX DOI=10.1126/JVI.74.8.3464-3469.2000;
 RA Liu B., Everson J.S., Fane B., Giannikopoulos P., Vreton E.,
 RA Lambden P.R., Clarke I.N.;
 RT "Molecular characterisation of a bacteriophage (Chp2) from Chlamydia
 RT peitraci".
 RL J. Virol. 74:3464-3469(2000).
 DR EMBL; AJ270057; CAB85589.1; -.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR003514; Capsid_F.
 DR Pfam; PF02305; Phage_F; 1.
 SQ SEQUENCE 565 AA; 63538 MW; 670485DC2A94932 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 497 ATSSLDS 503

RESULT 11

```
063CK1
ID 063CK1 PRELIMINARY; PRT; 586 AA.
AC 063CK1;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Multidrug ABC transporter, ATP-binding protein.
GN ORFName=BR2K1771;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18482.1; -.
KW ATP-binding.
SQ
SEQUENCE 586 AA; 64902 MW; BCE45D1F31C7CE7B CRC64;
OX NCBI_TaxID=180856;

Query Match 100.0%; Score 31; DB 2; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 12
ID 0739U8 PRELIMINARY; PRT; 586 AA.
AC 0739U8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ABC transporter, ATP-binding/permease protein.
GN OrderedLocNames=BCE2040;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Car R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Anguino S.V., Kolczay J.F.,
RA Nelson W.C., Koletsoe A.B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017270; AAS40963.1; -.
DR TIGR; BCE2040; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR01140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
```

```
SQ SEQUENCE 586 AA; 64869 MW; AA81400A8BA84193 CRC64;
OX NCBI_TaxID=180856;

Query Match 100.0%; Score 31; DB 2; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 13
ID 06HK05 PRELIMINARY; PRT; 586 AA.
AC 06HK05;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Multidrug resistance ABC transporter, ATP-binding and permease.
GN OrderedLocNames=BR9727_1789;
OS Bacillus thuringiensis (subsp. konjukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE017355; AAT59651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR01140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 586 AA; 64916 MW; 662AA920E116F5C4 CRC64;
OX NCBI_TaxID=180856;

Query Match 100.0%; Score 31; DB 2; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSLDS 7
DB 506 ATSSLDS 512

RESULT 14
ID 07PB25 PRELIMINARY; PRT; 589 AA.
AC 07PB25;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN Name=rib_Orf_420;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiinae; Rickettsia.
```

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OX NCBI_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereemeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AB001000001; EAA25659.1; -.
DR HSSP; Q9CHL8; 1MW5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR ATP-binding.
SQ SEQUENCE 589 AA; 67091 MW; 3E1FC057195F20DD CRC64;

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 511 ATSSLDS 517

RESULT 15
006967 PRELIMINARY; PRT; 589 AA.
AC 006967; Q795F6;
DT 01-JUN-1997 (TEMBLrel. 04, Created)
DT 01-JUN-1997 (TEMBLrel. 04, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Hypothetical protein yvcc.
GN Name=yvcc; OrderedLocustNames=BSU34820;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Denisot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denisot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Hénaut A.,
RA Hilbert H., Holappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kaashara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Königstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Maeda S., Manuel C.,
RA Médigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

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RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Ray M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scottone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shih B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassariotti A., Viati A., Wambut R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Zanchin A.;
RT "the complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; Z94043; CAB08051.1; -.
DR EMBL; Z99121; CAB15487.1; -.
DR PIR; D70031; D70031.
DR HSSP; Q9CHL8; 1MW5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Prodom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome; Hypothetical protein.
SQ SEQUENCE 589 AA; 64519 MW; 8A15163B5698DA08 CRC64;

```

```

Query Match 100.0%; Score 31; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 505 ATSSLDS 511

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Search completed: April 4, 2005, 15:56:14
Job time : 17.8307 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 17.9712 Seconds
(without alignments)
193.690 Million cell updates/sec

Title: US-09-887-853-6_COPY_222_230
Perfect score: 49
Sequence: 1 IQYAIFFPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038a:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 49 | 100.0 | 107 | 3 | AA90824 |
| 2 | 49 | 100.0 | 243 | 2 | AAW02280 |
| 3 | 49 | 100.0 | 243 | 2 | AAW53170 |
| 4 | 49 | 100.0 | 243 | 2 | AAW80424 |
| 5 | 49 | 100.0 | 243 | 7 | ABW00716 |
| 6 | 49 | 100.0 | 246 | 2 | AAW39569 |
| 7 | 49 | 100.0 | 267 | 4 | AAU04944 |
| 8 | 49 | 100.0 | 409 | 4 | AAU04945 |
| 9 | 44 | 89.8 | 534 | 2 | AAW39571 |
| 10 | 43 | 87.8 | 108 | 8 | AD126702 |
| 11 | 41 | 83.7 | 107 | 8 | AD25834 |
| 12 | 40 | 81.6 | 107 | 4 | AD25833 |
| 13 | 36 | 73.5 | 9 | 4 | AAW60407 |
| 14 | 36 | 73.5 | 9 | 4 | AAW61592 |
| 15 | 36 | 73.5 | 9 | 5 | AAW76520 |
| 16 | 36 | 73.5 | 9 | 5 | AAW15818 |
| 17 | 36 | 73.5 | 9 | 8 | ADJ788015 |
| 18 | 36 | 73.5 | 9 | 8 | ADJ788015 |
| 19 | 36 | 73.5 | 9 | 8 | ADN12061 |
| 20 | 36 | 73.5 | 9 | 8 | ADP43326 |
| 21 | 36 | 73.5 | 9 | 8 | ADJ18660 |
| 22 | 36 | 73.5 | 89 | 2 | AAW80080 |
| 23 | 36 | 73.5 | 92 | 2 | AAW95477 |
| 24 | 36 | 73.5 | 107 | 4 | AAW62083 |
| 25 | 36 | 73.5 | 107 | 4 | AAW62085 |

| | | | | | | |
|----|----|------|-----|---|----------|--------------------|
| 26 | 36 | 73.5 | 107 | 4 | AAW60398 | AAW60398 Humanised |
| 27 | 36 | 73.5 | 107 | 4 | AAW60396 | AAW60396 Mouse ant |
| 28 | 36 | 73.5 | 107 | 4 | AAW61583 | AAW61583 Humanised |
| 29 | 36 | 73.5 | 107 | 4 | AAW61581 | AAW61581 Murine 2C |
| 30 | 36 | 73.5 | 107 | 5 | AAW15812 | AAW15812 Human mAb |
| 31 | 36 | 73.5 | 107 | 6 | ABG74718 | ABG74718 Murine hu |
| 32 | 36 | 73.5 | 107 | 6 | ABG74702 | ABG74702 Murine hu |
| 33 | 36 | 73.5 | 107 | 6 | ABG74710 | ABG74710 Murine hu |
| 34 | 36 | 73.5 | 107 | 7 | ABW83149 | ABW83149 Hu007 ant |
| 35 | 36 | 73.5 | 107 | 7 | ABW83156 | ABW83156 Hu007 ant |
| 36 | 36 | 73.5 | 107 | 7 | ABW83157 | ABW83157 Hu007 ant |
| 37 | 36 | 73.5 | 107 | 7 | ABW83157 | ABW83157 Hu007 ant |
| 38 | 36 | 73.5 | 107 | 8 | AD271452 | AD271452 Humanise |
| 39 | 36 | 73.5 | 107 | 8 | AD271450 | AD271450 Murine mo |
| 40 | 36 | 73.5 | 107 | 8 | ADJ88006 | ADJ88006 Murine mo |
| 41 | 36 | 73.5 | 107 | 8 | ADJ88006 | ADJ88006 Humanised |
| 42 | 36 | 73.5 | 107 | 8 | ADN12050 | ADN12050 Variable |
| 43 | 36 | 73.5 | 107 | 8 | ADN12052 | ADN12052 Variable |
| 44 | 36 | 73.5 | 107 | 8 | ADP43326 | ADP43326 Humanised |
| 45 | 36 | 73.5 | 107 | 8 | ADP43324 | ADP43324 Murine an |
| | | | | | ADR73589 | ADR73589 Anti-AR a |

ALIGNMENTS

| | | |
|----------|--|----------------------------|
| RESULT 1 | AA90824 | standard; protein; 107 AA. |
| ID | AA90824 | standard; protein; 107 AA. |
| AC | AA90824; | |
| XX | | |
| DT | 29-AUG-2000 | (first entry) |
| XX | | |
| DE | 520C9 hybridoma VL domain SEQ ID NO:26. | |
| XX | | |
| KW | Antigen binding site; immunoglobulin; cancer antigen; immunological; | |
| KW | antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; | |
| KW | specific binding assay; affinity purification; drug targeting; | |
| KW | toxin targeting; imaging; genetic; therapeutic. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | US6054561-A. | |
| XX | | |
| PD | 25-APR-2000. | |
| XX | | |
| PF | 07-JUN-1995; | 95US-00483749. |
| XX | | |
| PR | 08-FEB-1984; | 84US-00577976. |
| PR | 11-JAN-1985; | 85US-00690750. |
| PR | 21-MAR-1986; | 86US-00842476. |
| PR | 08-MAY-1988; | 88US-00190778. |
| PR | 11-AUG-1994; | 94US-00288981. |
| XX | | |
| PA | (CHTR) CHIRON CORP. | |
| XX | | |
| PI | Ring DB; | |
| XX | | |
| DR | WPI; 2000-338508/29. | |
| DR | N-PSDB; AAA38908. | |
| XX | | |
| PT | Monoclonal antibody capable of binding to human breast cancer antigen | |
| PT | useful for affinity purification, drug or toxin targeting, imaging, and | |
| XX | treating cancer. | |
| PS | Disclosure; Fig 13; 57pp; English. | |
| XX | | |
| CC | The present invention describes a monoclonal antibody (Mab) (I) that | |
| CC | binds to a human breast cancer antigen that is also bound by Mab 454C11 | |
| CC | and 520C9 (produced by hybridoma ATCC HB8484 and HB8696, respectively). | |
| CC | described is a hybridoma that produces (I). (I) is useful in specific | |
| CC | binding assays, affinity purification, drug or toxin targeting, imaging, | |
| CC | and genetic or immunological therapeutics for various cancers. The | |

CC Present sequence represents a VL domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 49; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9
DB 89 LQYALFPYT 97

RESULT 2
ID AAM02280 standard; protein; 243 AA.

XX AAM02280;

XX 25-MAR-2003 (revised)
XX 29-OCT-1996 (first entry)

XX 520C9 anti-c-erbB-2 two single chain Fv construct.

XX 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;
XX construct; polypeptide linker; C-terminal amino acid sequence;
XX in vivo imaging; drug targeting experiment; homodimer; increased;
XX binding avidity; tissue retention time.

XX Homo sapiens.

XX Key Location/Qualifiers
XX FH 118.133
XX FT Peptide /label=linker

XX US5534254-A.

XX 09-JUL-1996.

XX 07-OCT-1993; 93US-00133804.

XX 06-FEB-1992; 92US-00831967.

XX (CHIR) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1996-333194/33.

XX N-PSDB; AAT36880.

XX Compns. contg. antigen-targeting antibody fragment constructs -
XX comprising dimer of single-chain Fv fragments.

XX Example 1; Col 33-36; 30pp; English.

XX Variable heavy (VH) and variable light (VL) genes were cloned from a
XX 520C9 hybridoma CDNA library, using probes directed toward the antibody
XX constant and joining regions. A two single chain Fv (sfv) gene was
XX constructed by connecting the VH and VL genes with a Ser rich polypeptide
XX linker. The resulting 520C9 two sfv gene, which encodes the present
XX sequence, was inserted into an expression vector, transformed into E.
XX coli, and protein expression induced by the addn. of IPTG to the culture
XX medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be
XX used for in vivo imaging, and drug targeting experiments. The 2 sfv
XX protein prod. is a homodimer, in which both fragments target the same
XX antigen, therefore giving greater binding avidity and longer tissue
XX retention times, compared to individual sfv protein prod. fragments.
XX (Updated on 25-MAR-2003 to correct FF field.)

XX Sequence 243 AA;

Query Match 100.0%; Score 49; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9
DB 222 LQYALFPYT 230

RESULT 3
ID AAM53170 standard; protein; 243 AA.

XX AAM53170;

XX 16-JUL-1998 (first entry)

XX 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

XX Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;
XX tumour; diagnosis; sg.

XX Synthetic.

XX Mus sp.

XX US5753204-A.

XX 19-MAY-1998.

XX 05-JUN-1995; 95US-00461838.

XX 06-FEB-1992; 92US-00831967.

XX 07-OCT-1993; 93US-00133804.

XX (CHIR) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Houston LL;

XX WPI; 1998-311318/27.

XX N-PSDB; AAV21798.

XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv
XX fragments.

XX Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)
XX construct. This was constructed by connecting the VH and VL genes with a
XX DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
XX antibody useful in targeting c-erbB-2 antigen. This dimeric construct can
XX be used in the methods of invention of imaging a preselected antigen
XX expressed in a mammal. The methods are used in magnetic resonance imaging
XX of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
XX constructs have enhanced properties as in vivo targeting agents in
XX comparison with intact monoclonal antibodies or their Fab fragments. The
XX dimeric constructs permit the in vivo targeting of an epitope on an
XX antigen with greater apparent avidity, including greater tumour
XX specificity, tumour localisation and tumour retention properties than
XX that of the Fab fragment having the same CDRs as the construct

XX Sequence 243 AA;

Query Match 100.0%; Score 49; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYALFPYT 9
DB 222 LQYALFPYT 230

RESULT 4

| | |
|-----------------------|---|
| AAW80424 | standard; protein; 243 AA. |
| ID | AAW80424 standard; protein; 243 AA. |
| XX | |
| AC | AAW80424; |
| XX | |
| DT | 28-JAN-1999 (first entry) |
| XX | |
| DE | 520C9 sFv sequence. |
| XX | |
| KW | 520C9 sFv; antigen; tumour cell; antibody 520C9; targeted delivery; |
| KW | antigen-expressing cell. |
| XX | |
| OS | Synthetic. |
| XX | |
| PN | US5837846-A. |
| XX | |
| PD | 17-NOV-1998. |
| XX | |
| EP | 05-JUN-1995; 95US-00461386. |
| XX | |
| XX | 06-FEB-1992; 92US-00831967. |
| PR | 07-OCT-1993; 93US-00133804. |
| XX | |
| PA | (CREA-) CREATIVE BIOMOLECULES INC. |
| PA | (CHIR) CHIRON CORP. |
| XX | |
| PI | Oppermann H, Houston LL, Huston JS, Ring DB; |
| XX | |
| DR | WPI, 1999-023541/02. |
| DR | N-P8DB; AAV63399. |
| XX | |
| PT | Nucleic acid encoding single-chain Fv fragment specific for antigens - |
| PT | and having C-terminal tail for crosslinking to form dimer with improved |
| PT | pharmacokinetic properties, used to deliver drugs and imaging agents, |
| PT | especially to tumours. |
| XX | |
| PS | Example 1; Col 35-36; 29pp; English. |
| XX | |
| CC | The present sequence represents an antibody 520C9 sFv. Variable heavy and |
| CC | light sequences of antibody 7520C9 are connected, together with a serine |
| CC | linker, to produce the present single chain Fv gene. The present sequence |
| CC | simplifies the invention. Dimers of the single chain Fv are used for |
| CC | targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs |
| CC | or 99m-technetium) to antigen-expressing cells, particularly for |
| CC | treatment or diagnosis of tumours (especially of ovary or breast) |
| XX | |
| SO | Sequence 243 AA; |
| XX | |
| Query Match | 100.0%; Score 49; DB 2; Length 243; |
| Best Local Similarity | 100.0%; Pred. No. 0.14; |
| Matches | 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| OY | 1 LOYALFPT 9 |
| | |
| DB | 222 LOYALFPT 230 |
| XX | |
| RESULT 5 | |
| ID | ABW00716 standard; protein; 243 AA. |
| XX | |
| AC | ABW00716; |
| XX | |
| DT | 15-JAN-2004 (first entry) |
| XX | |
| DE | 520C9 sFv protein. |
| XX | |
| KW | Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv; |
| KW | sFv. |
| XX | |
| OS | Unidentified. |
| XX | |
| PN | US2002168375-A1. |

```
XX 14-NOV-2002.
PD
XX
PF 21-JUN-2001; 2001US-00887853.
XX
PR 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-0013804.
PR 05-JUN-1995; 95US-00462641.
PR 26-APR-2000; 2000US-00558741.
XX
PA (CHIR ) CHIRON CORP.
XX
XX Huelton JS, Houelton LT, Ring DB, Oppermann H;
XX WPI; 2003-765156/72.
XX DR N-PSDB; AAD61485.
XX
PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
PS Example 1, Page 19-20; 30pp; English.
XX
XX The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preslected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibits cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 sfv protein. This sequence is used in the exemplification of the
XX invention
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 49; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LOVAIPPYT 9
DB 222 LOVAIPPYT 230
XX
RESULT 6
ID AAR39569 standard; protein; 246 AA.
XX
XX AAR39569;
XX AC
XX DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
DE Sequence of 520C9 sfv protein.
XX
XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW biosynthetic single polypeptide chain binding site; ss.
XX
OS Synthetic.
XX
XX WO9316185-A2.
XX PN
XX PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
PF XX
PR 06-FEB-1992; 92US-00831967.
PR XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU ) CETUS ONCOLOGY CORP.
XX
XX Huelton JS, Houelton LT, Ring DB, Oppermann H;
XX
```

DR WPI: 1993-272889/34.
DR N-PSDB; AAQ46084.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
XX imaging or treating breast or ovarian cancer etc.
PS Claim 4; Page 60-61; 87pp; English.
XX
CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AAQ46083, AAR39568). A single chain Fv (scFv) is a covalently
CC linked VH-VL heterodimer which is expressed from a gene fusion including
CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such
CC linker sequences are set forth in AA residues 116-135 in AAR39569, which
CC includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084
CC for the 520C9 monoclonal antibody, a single chain polypeptide can be
CC produced having a binding affinity for a C-erbB-2 related antigen. 'X' in
CC AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 246 AA;
SQ
Query Match 100.0%; Score 49; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;
OY 1 LQYAIFFPT 9
DB 222 LQYAIFFPT 230
RESULT 7
AAU04944
ID AAU04944 standard; protein; 267 AA.
XX
AC AAU04944;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
XX Humanised anti-p185 single chain antibody; 520C9H.
XX
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
KM cancer; tumour; adenocarcinoma.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key
FT 53. .57
FT Location/Qualifiers
FT /label= CDR
FT /note= "Complementarity determining region"
FT 72. .88
FT /label= CDR
FT /note= "Complementarity determining region"
FT 121. .126
FT /label= CDR
FT /note= "Complementarity determining region"
FT 138. .152
FT /label= Synthetic peptide linker
FT /note= "links the heavy chain to the light chain"
FT 176. .186
FT /label= CDR
FT /note= "Complementarity determining region"
FT 202. .208
FT /label= CDR
FT /note= "Complementarity determining region"
FT 241. .249
FT /label= CDR
FT /note= "Complementarity determining region"

FT Region 260. .267
FT /label= Glu_Glu_epitope
XX
XX MO200153354-A2.
XX
XX 26-UTL-2001.
XX
XX 19-JAN-2001; 2001WO-US001919.
XX
XX 20-JAN-2000; 2000US-0177258P.
XX
XX (CHTR) CHIRON CORP.
XX (HAMT-) HAMILTON CIVIC HOSPITALS RES DEV INC.
XX (HAMT-) HAMILTON REGIONAL CANCER CENT.
XX
XX Austin R, Kwok CS, Ring DB;
XX
XX WPI: 2001-451904/48.
XX N-PSDB; AAS09507.
XX
XX Novel immunoconjugate useful for inhibiting tumor cell growth in vivo
XX comprises a humanized anti-p185 antibody linked to an interleukin-2
XX polypeptide.
XX
XX Claim 7; Fig 9; 74pp; English.
XX
XX The sequence represents a humanised anti-p185 single chain antibody which
XX is linked to a human interleukin-2 (IL-2) molecule to make a fusion
XX protein. The fusion protein (or immunoconjugate) is used to inhibit the
XX growth of tumours or cancers particularly those characterised by
XX overexpression of p185 e.g. human adenocarcinomas and malignant and/or
XX benign tumours of the breast, renal system, salivary gland,
XX gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
XX correct OS field.)
SQ Sequence 267 AA;
SQ
Query Match 100.0%; Score 49; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;
OY 1 LQYAIFFPT 9
DB 241 LQYAIFFPT 249
RESULT 8
AAU04945
ID AAU04945 standard; protein; 409 AA.
XX
AC AAU04945;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
XX Humanised anti-p185 antibody/IL-2 fusion protein.
XX
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
KM cancer; tumour; adenocarcinoma; fusion protein.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key
FT 1. .22
FT Location/Qualifiers
FT /label= Signal_peptide
FT 23. .409
FT /label= Mature_fusion_protein
FT 23. .259
FT /label= Humanised_antibody_520C9H
FT 53. .57
FT Region

| Query Match | Best Local Similarity | Score 49; | DB 4; | Length 409; |
|------------------|-----------------------|---------------|-----------|-------------|
| Matches 9; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| 1 LOYALPYT 9 | | | | |
| 241 LOYALPYT 249 | | | | |

RESULT 9

| | | |
|-----------|---|----------------------------|
| ID | AA039571 | standard; protein; 534 AA. |
| XX | AA039571; | |
| AC | AA039571; | |
| XX | | |
| DT | 25-MAR-2003 (revised) | |
| DT | 07-FEB-1994 (first entry) | |
| XX | | |
| DE | Sequence of G-FIT. | |
| XX | | |
| KW | Tumour antigen; c-erbB-2; G-FIT. | |
| XX | | |
| OS | Synthetic. | |
| XX | | |
| PN | W09J16185-A2. | |
| XX | | |
| PD | 19-AUG-1993. | |
| XX | | |
| PF | 05-FEB-1993; 93WO-US001055. | |
| PR | 06-FEB-1992; 92US-00831967. | |
| XX | | |
| PA | (CREA-) CREATIVE BIOMOLECULES INC. (CETU) CETUS ONCOLOGY CORP. | |
| XX | | |
| PI | Hueton JS, Hueton LL, Ring DB, Oppermann H; WP1; 1993-272889/34. | |
| DR | N-PSDB; AAQ46086. | |
| XX | | |
| PT | New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for imaging or treating breast or ovarian cancer etc. | |
| XX | | |
| PS | Example; Page 65-68; 87pp; English. | |
| CC | | |
| CC | c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. Such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about 5.3 (see AAQ46083, AAR39568). (Updated on 25-MAR-2003 to correct PN field.) | |
| CC | | |
| XX | | |
| SQ | Sequence 534 AA; | |
| QY | | |
| Db | 1 LQYAIPFYT 9 513 LQYPIFPYT 521 | |
| RESULT 10 | | |
| AD126702 | | |
| ID | AD126702 standard; protein; 108 AA. | |
| XX | | |
| AC | AD126702; | |
| XX | | |
| DT | 15-APR-2004 (first entry) | |
| XX | | |
| DE | Mouse anti IGM antibody HNK-1 kappa light chain protein. | |
| XX | | |
| KW | Mouse; antibody; IGM; remyelination; neuronal growth; autoantibody; demyelination disease; multiple sclerosis; central nervous system; CNS; axon; glial cell proliferation; Theiler's murine encephalomyelitis virus infection; CNS injury; spinal cord injury. | |
| XX | | |
| OS | Mus sp. | |
| XX | | |
| PN | US2003185827-A1. | |
| XX | | |
| PD | 02-OCT-2003. | |

| | | | | | |
|-----------------------|---|--|--|--|--|
| XX | 13-NOV-2001; 2001US-00010729. | | | | |
| PF | | | | | |
| XX | 29-APR-1994; 94US-00235520. | | | | |
| XX | 08-AUG-1996; 96US-00692084. | | | | |
| PR | 07-JAN-1997; 97US-00779784. | | | | |
| PR | 28-MAY-1997; 99US-00322862. | | | | |
| PR | 30-MAY-2000; 2000US-00580787. | | | | |
| PR | 05-DEC-2000; 2000US-00730473. | | | | |
| XX | | | | | |
| XX | (MAYO-) MAYO FOUND. | | | | |
| XX | | | | | |
| XX | Rodriguez M, Miller DJ, Pease LR; | | | | |
| DR | WPI; 2004-119219/12. | | | | |
| DR | N-PSDB; ADI26703. | | | | |
| XX | | | | | |
| XX | New human immunoglobulin M antibody for treating or preventing a | | | | |
| PT | demyelinating disease of the central nervous system in a human or | | | | |
| PT | domestic animal, such as multiple sclerosis. | | | | |
| XX | | | | | |
| PS | Example 19; Fig 69; 159p; English. | | | | |
| XX | | | | | |
| CC | The invention relates to an antibody (I) produced by injecting an | | | | |
| CC | immunocompetent host with an antibody peptide, and harvesting the | | | | |
| CC | antibody, where the peptide comprises a human anti-IgM antibody fragment | | | | |
| CC | given in the specification, or active fragments. Also included are | | | | |
| CC | stimulating remyelination of central nervous system (CNS) axons in a | | | | |
| CC | mammal (comprising administering a monoclonal antibody, or mixtures, | | | | |
| CC | monomers, active fragments, or recombinant antibodies derived from it, | | | | |
| CC | characterised by their ability to bind structures and cells within the | | | | |
| CC | CNS, including oligodendrocytes), stimulating the proliferation of glial | | | | |
| CC | cells in CNS axons in a mammal (comprising administering a monoclonal | | | | |
| CC | antibody, or mixtures, monomers, active fragments, or recombinant | | | | |
| CC | antibodies derived from it, characterised by their ability to bind | | | | |
| CC | structures and cells within the CNS), treating or preventing a | | | | |
| CC | demyelinating disease of the CNS in a mammal (comprising administering a | | | | |
| CC | monoclonal antibody, or mixtures, monomers, active fragments, or | | | | |
| CC | recombinant antibodies derived from it, characterised by their ability to | | | | |
| CC | bind structures and cells within the CNS, and to stimulate remyelination | | | | |
| CC | of axons of the CNS), stimulating, in vitro, the proliferation of glial | | | | |
| CC | cells from mixed cell culture, stimulating remyelination of CNS axons in | | | | |
| CC | a mammal, a DNA sequence (or degenerate variant of it) which encodes an | | | | |
| CC | antibody (or a peptide analogue, hapten, or active fragment of it, where | | | | |
| CC | the DNA sequence consists of a sequence encoding an anti IgM antibody), a | | | | |
| CC | probe capable of screening for the antibody, an assay for screening drugs | | | | |
| CC | and other agents for the ability to modulate the production or mimic the | | | | |
| CC | activities of mAb SH1GM22, SH1GM45, or combinations of them, a | | | | |
| CC | recombinant virus transformed with recombinant antibody nucleic acids or | | | | |
| CC | vector, imaging a portion of the CNS using the antibody and diagnosing or | | | | |
| CC | monitoring demyelination and/or remyelination of the CNS comprising using | | | | |
| CC | CNS image. The antibody is used to stimulate remyelination of CNS axons, | | | | |
| CC | and to stimulate the proliferation of glial cells in CNS axons, | | | | |
| CC | optionally in vitro. The antibody is used to treat or prevent a | | | | |
| CC | demyelinating disease of the CNS in a human or domestic animal, such as | | | | |
| CC | multiple sclerosis, or a disease, other injury or dysfunction of the CNS, | | | | |
| CC | preferably the mammal is a mouse infected with Strain DA of Theiler's | | | | |
| CC | murine encephalomyelitis virus. The antibody is used to treat a spinal | | | | |
| CC | cord injury and used to screen drugs and other agents for the ability to | | | | |
| CC | modulate the production or mimic the activities of the antibody. The | | | | |
| CC | antibody can be used to image a portion of the CNS which can be used to | | | | |
| CC | diagnose or monitor demyelination and/or remyelination of the CNS. The | | | | |
| CC | present sequence is a variable region of a mouse anti-IgM antibody (or | | | | |
| CC | fragment). | | | | |
| XX | | | | | |
| XX | Sequence 108 AA; | | | | |
| XX | | | | | |
| Query Match | 87.8%; Score 43; DB 8; Length 108; | | | | |
| Best Local Similarity | 86.9%; Pred. NO. 0.93; | | | | |
| Matches | 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0 | | | | |
| 1 | LOVAIFPYT 9 | | | | |

| | | |
|----|--|-------------|
| Db | 89 | LQVASFPT 97 |
| XX | RESULT 11 | |
| XX | ADE25834 | |
| ID | ADE25834 standard; protein; 107 AA. | |
| XX | | |
| XX | ADE25834; | |
| XX | | |
| XX | 26-FEB-2004 (first entry) | |
| XX | | |
| DE | Anti-alpha-v-beta-6 monoclonal Ab light chain variable domain SEQ ID:41. | |
| XX | | |
| KW | monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP; | |
| KW | cytostatic; dermatological; vulnery; hepatotropic; immunosuppressive; | |
| KW | vaccine; fibrosis; scleroderma; scarring; liver fibrosis; | |
| XX | kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome. | |
| OS | Synthetic. | |
| XX | | |
| XX | WO2003100033-A2. | |
| PD | | |
| PD | 04-DEC-2003. | |
| XX | | |
| PF | 13-MAR-2003; 2003WO-US008048. | |
| XX | | |
| PR | 13-MAR-2002; 2002US-0364891P. | |
| PR | 13-NOV-2002; 2002US-0426286P. | |
| XX | | |
| PA | (BIOJ) BIOGEN INC. | |
| PA | (REGC) UNIV CALIFORNIA. | |
| XX | | |
| PI | Violette SM, Weinreb PH, Simon KJ, Shepard D, Leone DR; | |
| XX | | |
| XX | WPI; 2004-035139/03. | |
| DR | | |
| XX | | |
| PT | New monoclonal antibody that specifically binds to alpha-v-beta-6, and | |
| PT | inhibits the binding of alpha v beta 6 to latency associated peptide | |
| PT | (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's | |
| PT | syndrome. | |
| XX | | |
| XX | | |
| XX | | |
| PS | Claim 27; SEQ ID NO 41; 83pp; English. | |
| XX | | |
| XX | The present invention describes a monoclonal antibody (1) that | |
| CC | specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v- | |
| CC | -beta-6 to latency associated peptide (LAP) with an IC50 value lower than | |
| CC | that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody | |
| CC | comprising heavy chain complementarity determining regions (CDR) 1, 2, | |
| CC | and 3, or a heavy and light chain variable domain sequence; (2) a | |
| CC | monoclonal antibody that specifically binds to alpha-v-beta-6 but does | |
| CC | not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for | |
| CC | preventing or treating a disease mediated by alpha-v-beta-6 in a mammal | |
| CC | comprising the antibody and a carrier; (4) a method for treating a | |
| CC | subject having or at risk of having a disease mediated by alpha-v-beta-6 | |
| CC | by administering to the subject the composition described above, and so | |
| CC | alleviating or postponing the onset of the disease; (5) a method of | |
| CC | detecting alpha-v-beta-6 in a tissue sample by contacting the tissue | |
| CC | sample with the antibody; and (6) a cell hybridoma 6.1A6; 6.3G3; 6.8G6; | |
| CC | 6.2B1; 7.1G10; 7.7G5; or 7.1C1, which respectively comprise American | |
| CC | Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA- | |
| CC | 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytostatic, | |
| CC | dermatological, vulnery, hepatotropic and immunosuppressive activities; | |
| CC | and can be used in vaccines. The antibodies, compositions and methods of | |
| CC | the present invention can be used for preventing or treating a disease | |
| CC | mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring, | |
| CC | liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer, | |
| CC | preferably epithelial cancer, oral, skin, cervical, pharyngeal, | |
| CC | laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or | |
| CC | Alport's syndrome. The present sequence is used in the exemplification of | |
| CC | the present invention. | |
| XX | | |
| XX | Sequence 107 AA; | |
| XX | | |

Query Match 83.7%; Score 41; DB 8; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQYAFPYT 9
|||:|
DB 89 LQYATPYT 97

RESULT 12
ADE25833
ID ADE25833 standard; protein; 107 AA.
XX ADE25833;
AC
XX 26-FEB-2004 (first entry)
DT
XX
DE Anti-alpha-v-beta-6 monoclonal Ab light chain variable domain SEQ ID:40.
XX
XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
XX cytostatic; dermatological; vulnery; hepatocytic; immunosuppressive;
XX vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
XX kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
XX
XX Synthetic.
XX
XX WO2003100033-A2.
XX
XX 04-DEC-2003.
XX
XX 13-MAR-2003; 2003WO-US008048.
XX
XX 13-MAR-2002; 2002US-0364991P.
XX 13-NOV-2002; 2002US-0426286P.
XX
XX (BIOJ) BIOGEN INC.
XX (RECC) UNIV CALIFORNIA.
XX
XX Violante SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
XX WPI; 2004-035139/03.
XX
XX
XX Claim 26; SEQ ID NO 40; 83pp; English.

CC The present invention describes a monoclonal antibody (1) that
CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
CC -beta-6 to latency associated peptide (LAP) with an IC50 value lower than
CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
CC comprising heavy chain complementarily determining regions (CDR) 1, 2,
CC and 3, or a heavy and light chain variable domain sequence; (2) a
CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
CC comprising the antibody and a carrier; (4) a method for treating a
CC subject having or at risk of having a disease mediated by alpha-v-beta-6
CC by administering to the subject the composition described above, and so
CC alleviating or postponing the onset of the disease; (5) a method of
CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
CC 6.2B1, 7.1G10, 7.7G5, or 7.1CR, which respectively comprises American
CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytostatic,
CC dermatological, vulnery, hepatocytic and immunosuppressive activities,
CC and can be used in vaccines. The antibodies, compositions and methods of
CC the present invention can be used for preventing or treating a disease
CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,

CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
CC Alport's syndrome. The present sequence is used in the exemplification of
CC the present invention.
XX
XX SQ Sequence 107 AA;

Query Match 81.6%; Score 40; DB 8; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LQYAFPYT 9
|||:|
DB 89 LQYATPYT 97

RESULT 13
AAB60407
ID AAB60407 standard; peptide; 9 AA.
XX AAB60407;
AC
XX 24-APR-2001 (first entry)
DT
XX
DE ErbB2-reactive VL CDR, SEQ ID NO:12.
XX
XX Anti-ErbB2 monoclonal antibody; HER2; humanised; VL;
XX light chain variable region; cancer; cytostatic; EGFR-expressing cancer;
XX epidermal growth factor receptor; colon cancer; rectal cancer; tumour;
XX colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
XX affinity purification; complementarily determining region; CDR.
XX
XX Mus musculus.
XX
XX WO200100245-A2.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US017366.
XX
XX 25-JUN-1999; 99US-014316P.
XX
XX (GETH) GENENTECH INC.
XX Adams CW, Presta LG, Sliwkowsky M;
XX WPI; 2001-080862/09.
XX
XX
XX Claim 46; Page 66; 89pp; English.

CC The invention relates to a method for treating cancer in a human patient,
CC wherein the cancer expresses epidermal growth factor receptor (EGFR),
CC comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody
CC 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398,
CC AAB60399). The invention also encompasses an isolated nucleic acid
CC encoding a humanised ErbB2-binding antibody; vectors and host cells
CC comprising such nucleic acids; the recombinant production of a humanised
CC ErbB2-binding antibody; and an immunocjugate comprising a humanised
CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies
CC act by antagonising ErbB receptors, and as inhibitors of transforming
CC growth factor alpha (TGF-alpha)-activated mitogen activated protein
CC kinase (MAPK). The method of the invention is used for treating cancer,
CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer,
CC (especially non-small cell lung cancer), or breast cancer (especially
CC metastatic breast cancer). The antibodies may also have non-therapeutic
CC uses e.g., as affinity purification agents. Using an antibody which binds
CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted
CC drugs, as EGFR is also highly expressed in other tissues such as the
CC liver and skin, where the active drug will also bind, with skin toxicity

CC having been observed for EGFR-targeted drugs. Antibodies which bind
 CC ErbB2 are anticipated to have a better safety profile than such drugs.
 CC The present sequence represents a specifically claimed light chain
 CC variable region (VL) complementarily determining region (CDR) of a
 CC humanised anti-ErbB2 antibody of the invention
 CC
 XX
 SQ Sequence 9 AA;

Query Match 73.5%; Score 36; DB 4; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9
 DB 2 QYIYFPT 9

RESULT 14
 AAB61592
 ID AAB61592 standard; peptide; 9 AA.

AC AAB61592;

DT 04-APR-2001 (first entry)

DE Humanised Fab version 574 variable light chain CDR #3.

XX ErbB2; cytosolic; prostate cancer; receptor tyrosine kinase; antibody;
 XX ErbB receptor; monoclonal antibody 2C4; variable light chain;
 KW complementarity determining region; CDR.

XX Unidentified.

OS WO200100238-A1.

XX 04-JUN-2001.

PD 23-JUN-2000; 2000WO-US017423.

PF 25-JUN-1999; 99US-0141315P.

XX (GETH) GENENTECH INC.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX Agus DB, Scher HI, Sliwkowski MX;

XX WPI; 2001-159131/16.

PT Treating prostate cancer in a human comprises administering an antibody
 PT which binds ErbB2 and blocks ligand activation of an ErbB receptor.

XX Disclosure; Page 24; 93pp; English.

CC The ErbB family of receptor tyrosine kinases are important mediators of
 CC cell growth, differentiation and survival. The receptor family includes
 CC four distinct members including Epidermal Growth Factor Receptor (EGFR or
 CC ErbB1), HER2 (ErbB2 or p185 neu), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).
 CC The present invention relates to a method for treating prostate cancer.
 CC The method comprises administering an antibody which binds ErbB2 and
 CC blocks ligand activation of an ErbB receptor. Preferably, the antibody
 CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
 CC alpha activation of mitogen-activated protein kinase (MAPK). The present
 CC sequence is a complementarity determining region (CDR) from the variable
 CC light chain of humanised Fab version 574 antibody
 CC
 XX

SO Sequence 9 AA;

Query Match 73.5%; Score 36; DB 4; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9
 DB 2 QYIYFPT 9

DB 2 QYIYFPT 9

RESULT 15
 AAU76520

ID AAU76520 standard; peptide; 9 AA.

AC AAU76520;

DT 05-JUN-2002 (first entry)

DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-Interleukin-12; CDR; light chain; circulatory;
 KW complementarity determining region; neuroprotective; antiproliferative;
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
 KW neurological disorder.

XX Homo sapiens.

OS WO200212500-A2.

PD 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US024720.

XX 07-AUG-2000; 2000US-023358P.

PR 29-SEP-2000; 2000US-0236827P.

PR 01-AUG-2001; 2001US-00920262.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Perritt D, Scallion B, Shealy D;

XX WPI; 2002-257482/30.

PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL
 PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as
 PT other for treating immune, infectious, malignant or neurological
 PT disorders.

XX Claim 41; Page 93; 96pp; English.

CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL
 CC -12) antibodies. The antibodies comprise at least one complementarity
 CC determining region (CDR) of a heavy or light chain, a heavy chain or
 CC light chain variable region, or a heavy chain or light chain constant
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
 CC The antibodies are also useful for treating immune, cardiovascular,
 CC infectious, malignant or neurological disorders or diseases. The present
 CC sequence represents the amino acid sequence of human anti-interleukin-12
 CC (IL-12) antibody CDR3 light chain
 CC
 XX

SO Sequence 9 AA;

Query Match 73.5%; Score 36; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPT 9
 DB 2 QYIYFPT 9

Search completed: April 4, 2005, 15:47:18
 Job time : 18.9712 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 13.2843 Seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_222_230

Perfect score: 49

Sequence: 1 LOYAFPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|-------|----------------------|
| 1 | 49 | 100.0 | 243 | 9 | US-09-887-853-6 |
| 2 | 49 | 100.0 | 243 | 17 | US-10-683-547-6 |
| 3 | 49 | 100.0 | 267 | 9 | US-09-766-543-10 |
| 4 | 49 | 100.0 | 276 | 9 | US-09-766-543-12 |
| 5 | 43 | 87.8 | 108 | 14 | US-10-010-729-45 |
| 6 | 39 | 79.6 | 217 | 16 | US-10-437-963-119518 |
| 7 | 36 | 73.5 | 9 | 10 | US-09-920-262A-6 |
| 8 | 36 | 73.5 | 9 | 14 | US-10-268-501-12 |
| 9 | 36 | 73.5 | 9 | 15 | US-10-608-626-12 |
| 10 | 36 | 73.5 | 9 | 16 | US-10-912-994-6 |
| 11 | 36 | 73.5 | 88 | 16 | US-10-437-963-117213 |
| 12 | 36 | 73.5 | 107 | 14 | US-10-268-501-1 |
| 13 | 36 | 73.5 | 107 | 14 | US-10-268-501-3 |

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| 14 | 36 | 73.5 | 107 | 15 | US-10-608-626-1 | Sequence 1, Appli |
| 15 | 36 | 73.5 | 107 | 15 | US-10-608-626-3 | Sequence 3, Appli |
| 16 | 36 | 73.5 | 107 | 15 | US-10-600-152-10 | Sequence 10, Appl |
| 17 | 36 | 73.5 | 107 | 15 | US-10-600-152-12 | Sequence 12, Appl |
| 18 | 36 | 73.5 | 107 | 16 | US-10-619-754-1 | Sequence 1, Appli |
| 19 | 36 | 73.5 | 107 | 16 | US-10-619-754-3 | Sequence 3, Appli |
| 20 | 36 | 73.5 | 107 | 17 | US-10-877-532-3 | Sequence 3, Appli |
| 21 | 36 | 73.5 | 108 | 17 | US-09-920-262A-8 | Sequence 8, Appli |
| 22 | 36 | 73.5 | 108 | 16 | US-10-912-994-8 | Sequence 8, Appli |
| 23 | 36 | 73.5 | 109 | 9 | US-09-811-123-4 | Sequence 4, Appli |
| 24 | 36 | 73.5 | 109 | 9 | US-09-811-123-5 | Sequence 5, Appli |
| 25 | 36 | 73.5 | 622 | 16 | US-10-437-963-183264 | Sequence 183264, |
| 26 | 35 | 71.4 | 9 | 9 | US-09-861-294-10 | Sequence 10, Appl |
| 27 | 35 | 71.4 | 9 | 9 | US-09-924-099-5 | Sequence 5, Appli |
| 28 | 35 | 71.4 | 9 | 14 | US-10-367-506-10 | Sequence 10, Appl |
| 29 | 35 | 71.4 | 69 | 14 | US-10-106-698-7392 | Sequence 7392, Ap |
| 30 | 35 | 71.4 | 94 | 15 | US-10-424-559-270138 | Sequence 270138, |
| 31 | 35 | 71.4 | 107 | 15 | US-10-412-703A-12 | Sequence 12, Appl |
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| 33 | 35 | 71.4 | 108 | 15 | US-10-412-703A-6 | Sequence 6, Appli |
| 34 | 35 | 71.4 | 130 | 8 | US-08-779-784-35 | Sequence 35, Appl |
| 35 | 35 | 71.4 | 130 | 14 | US-10-010-729-71 | Sequence 71, Appl |
| 36 | 35 | 71.4 | 145 | 9 | US-09-861-294-2 | Sequence 2, Appli |
| 37 | 35 | 71.4 | 145 | 14 | US-10-367-506-2 | Sequence 2, Appli |
| 38 | 35 | 71.4 | 236 | 17 | US-10-879-994-6 | Sequence 6, Appli |
| 39 | 35 | 71.4 | 237 | 9 | US-09-924-099-9 | Sequence 9, Appli |
| 40 | 35 | 71.4 | 243 | 9 | US-09-924-099-10 | Sequence 10, Appl |
| 41 | 35 | 71.4 | 257 | 15 | US-10-239-656-55 | Sequence 55, Appl |
| 42 | 35 | 71.4 | 257 | 15 | US-10-239-656-67 | Sequence 67, Appl |
| 43 | 35 | 71.4 | 499 | 15 | US-10-239-656-73 | Sequence 73, Appl |
| 44 | 34 | 69.4 | 82 | 15 | US-10-424-559-246038 | Sequence 246038, |
| 45 | 34 | 69.4 | 107 | 15 | US-10-389-155-9 | Sequence 9, Appli |

ALIGNMENTS

RESULT 1

US-09-887-853-6

Sequence 6, Application US/09887853

Patent No. US20020168375A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

Oppermann, Hermann

Houston, L. L.

Ring, David B.

TITLE OF INVENTION: Biochemical Binding Proteins For Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSER: Testa, Hurwitz & Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 243 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match      100.0%; Score 49; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      222 LOYALFPYT 230

RESULT 2
US-10-683-547-6
; Sequence 6, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
; APPLICANT: Huston, J.
; APPLICANT: Houston, L.L.
; APPLICANT: Ring, D.
; APPLICANT: Oppermann, H.
; TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
; FILE REFERENCE: CIB-P01-130
; CURRENT APPLICATION NUMBER: US/10/683,547
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/09/558,741
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 07/831,967
; PRIOR FILING DATE: 1992-02-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 520C9 sfv
US-10-683-547-6

Query Match      100.0%; Score 49; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      222 LOYALFPYT 230

RESULT 3
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwock, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679, 002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
```

```

;
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match      100.0%; Score 49; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      241 LOYALFPYT 249

RESULT 4
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwock, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679, 002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match      100.0%; Score 49; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOYALFPYT 9
DB      241 LOYALFPYT 249

RESULT 5
US-10-010-729-45
; Sequence 45, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
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;; PRIOR FILING DATE: 1997-01-07
;; PRIOR APPLICATION NUMBER: 08/692,084
;; PRIOR FILING DATE: 1996-08-09
;; PRIOR APPLICATION NUMBER: 08/236,520
;; PRIOR FILING DATE: 1994-04-29
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: FaSTSeq for Windows Version 4.0
;; SEQ ID NO 45
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-010-729-45

Query Match 87.8%; Score 43; DB 14; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALPYT 9
|||:||||
DB 89 LOYASFPYT 97

RESULT 6
US-10-437-963-119518
; Sequence 119518, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119518
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22728C.1.pep
US-10-437-963-119518

Query Match 79.6%; Score 39; DB 16; Length 217;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAIFFPYT 9
|||:||||
DB 199 YAVFPYT 205

RESULT 7
US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358

;; PRIOR FILING DATE: 2000-08-07
;; PRIOR APPLICATION NUMBER: 60/236,827
;; PRIOR FILING DATE: 2000-09-29
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver 3.1
;; SEQ ID NO 6
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-920-262A-6

Query Match 73.5%; Score 36; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPYT 9
|||:||||
DB 2 QYNIFFPYT 9

RESULT 8
US-10-268-501-12
; Sequence 12, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-268-501-12

Query Match 73.5%; Score 36; DB 14; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFPYT 9
|||:||||
DB 2 QYIIFPYT 9

RESULT 9
US-10-608-626-12
; Sequence 12, Application US/10608626
; Publication No. US20040013667A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-608-626-12

Query Match 73.5%; Score 36; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFYT 9
Db 2 QYIYIYPT 9

RESULT 10

US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US20050002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIV1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-994-6

Query Match 73.5%; Score 36; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFYT 9
Db 2 QYIYIYPT 9

RESULT 11

US-10-437-963-137213
; Sequence 137213, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbasuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 137213
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38717C.1.pep
US-10-437-963-137213

Query Match 73.5%; Score 36; DB 16; Length 88;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VAIFFYT 9
Db 60 FAIFFYT 66

RESULT 12

US-10-268-501-1
; Sequence 1, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-268-501-1

Query Match 73.5%; Score 36; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFYT 9
Db 90 QYIYIYPT 97

RESULT 13

US-10-268-501-3
; Sequence 3, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized VL sequence
US-10-268-501-3

Query Match 73.5%; Score 36; DB 14; Length 107;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIFFYT 9
Db 90 QYIYIYPT 97

RESULT 14

US-10-608-626-1
; Sequence 1, Application US/10608626
; Publication No. US20040013667A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-608-626-1

Query Match 73.5%; Score 36; DB 15; Length 107;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QYAIFFPYT 9
|||:||||
Db 90 QYIYIPYT 97

RESULT 15
US-10-608-626-3
; Sequence 3, Application US/10608626
; Publication No. US20040013667A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized VL sequence
US-10-608-626-3

Query Match 73.5%; Score 36; DB 15; Length 107;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QYAIFFPYT 9
|||:||||
Db 90 QYIYIPYT 97

Search completed: April 4, 2005, 16:42:45
Job time : 13.2843 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 3.2492 Seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_222_230
Perfect score: 49
Sequence: 1 LQYAFPPY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1 | 39 | 79.6 | 450 | 2 | F69371 | bile acid-inducibl |
| 2 | 36 | 73.5 | 106 | 2 | S20652 | Ig kappa chain V r |
| 3 | 36 | 73.5 | 107 | 2 | E64356 | conserved hypochet |
| 4 | 36 | 73.5 | 177 | 2 | S62520 | hypothetical prote |
| 5 | 35 | 71.4 | 98 | 2 | PH1062 | Ig light chain V r |
| 6 | 35 | 71.4 | 101 | 2 | C28840 | Ig kappa chain V r |
| 7 | 35 | 71.4 | 101 | 2 | B28840 | Ig kappa chain V r |
| 8 | 35 | 71.4 | 106 | 2 | PL0262 | Ig kappa chain V r |
| 9 | 35 | 71.4 | 108 | 1 | K1HUM7 | Ig kappa chain V-I |
| 10 | 34 | 69.4 | 398 | 2 | C71857 | probable lipopolys |
| 11 | 34 | 69.4 | 416 | 2 | T50279 | hypothetical berin |
| 12 | 34 | 69.4 | 431 | 2 | A64658 | LPS biosynthesis p |
| 13 | 33 | 67.3 | 97 | 2 | H84019 | hypothetical prote |
| 14 | 33 | 67.3 | 107 | 2 | F83707 | hypothetical prote |
| 15 | 33 | 67.3 | 117 | 2 | S42466 | Ig kappa chain V r |
| 16 | 33 | 67.3 | 129 | 2 | B23986 | Ig kappa chain pre |
| 17 | 33 | 67.3 | 172 | 2 | AB1268 | cell-shape determi |
| 18 | 33 | 67.3 | 172 | 2 | AD1630 | cell-shape determi |
| 19 | 33 | 67.3 | 242 | 2 | AB3523 | taurine transporter |
| 20 | 33 | 67.3 | 642 | 2 | F83718 | ABC transporter (A |
| 21 | 33 | 67.3 | 21 | 2 | T28847 | hypothetical prote |
| 22 | 33 | 67.3 | 2139 | 2 | S46404 | vitellogenin - yel |
| 23 | 32.5 | 66.3 | 723 | 2 | AC1241 | polynucleotide pho |
| 24 | 32.5 | 66.3 | 723 | 2 | AG1603 | polynucleotide pho |
| 25 | 32 | 65.3 | 106 | 2 | UQ0234 | hypothetical 12.5k |
| 26 | 32 | 65.3 | 108 | 1 | K1HUKU | Ig kappa chain V-I |
| 27 | 32 | 65.3 | 112 | 2 | B49060 | Ig light chain V r |
| 28 | 32 | 65.3 | 127 | 2 | S52447 | Ig kappa chain V r |
| 29 | 32 | 65.3 | 149 | 2 | B69225 | hypothetical prote |

| | | | | | | |
|----|----|------|-----|---|--------|---------------------|
| 30 | 32 | 65.3 | 160 | 2 | H86162 | hypothetical prote |
| 31 | 32 | 65.3 | 210 | 2 | B81011 | glyoxalase II faml |
| 32 | 32 | 65.3 | 218 | 2 | F97021 | ABC transporter, p |
| 33 | 32 | 65.3 | 251 | 2 | I40671 | flir protein - Cau |
| 34 | 32 | 65.3 | 299 | 2 | G82393 | transcription regu |
| 35 | 32 | 65.3 | 331 | 2 | T45089 | pyruvate synthase |
| 36 | 32 | 65.3 | 334 | 2 | F75046 | pyruvate synthase |
| 37 | 32 | 65.3 | 334 | 2 | F71114 | probable ferredoxi |
| 38 | 32 | 65.3 | 371 | 2 | D90192 | alcohol dehydrogen |
| 39 | 32 | 65.3 | 401 | 2 | S37815 | autooxidation A res |
| 40 | 32 | 65.3 | 412 | 2 | T41552 | hypothetical prote |
| 41 | 32 | 65.3 | 427 | 2 | F75169 | serine hydroxymeth |
| 42 | 32 | 65.3 | 427 | 2 | F71045 | probable serine hy |
| 43 | 32 | 65.3 | 458 | 2 | C69406 | methylmalonyl-CoA |
| 44 | 32 | 65.3 | 481 | 2 | D75596 | UDP-galactose-1-epi |
| 45 | 32 | 65.3 | 508 | 2 | S73859 | pyruvate kinase (E |

ALIGNMENTS

RESULT 1
F69371
bile acid-inducible operon protein F (baif-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jul-2004
C/Accession: F69371
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaune, B.P.; Sykes, S.A. Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: F69371
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-450 <KLB>
A:Cross-references: UNIPROT:O29288; GB:AE001037; GB:AE000782; NID:G2689360; PIDN:AAB9026;

Query Match 79.6%; Score 39; DB 2; Length 450;
Best Local Similarity 85.7%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPPY 9
||:||||
Db 275 YAFPPY 281

RESULT 2
S20652
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S20652
R/Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
A:Submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacti
A:Reference number: S20639
A:Accession: S20652
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <LO6>
A:Cross-references: EMBL:X65008; NID:G52649; PIDN:CAA46141.1; PID:G52650
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 36; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 89 LOYDDFPYT 97

RESULT 3

E64356

Conserved hypothetical protein MJ0453 - Methanococcus jannaschii

C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C/Accession: E64356
R/Built: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Oerbeck, R.; Kirkness, E.F.; Weinstein, K.G.; Merrick, J.M.; Glodok, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hult, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:9637999; PMID:868087
A/Accession: E64356
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-107 <BUL>
A/Cross-references: UNIPROT:Q57895; GB:U67496; GB:L77117; NID:g2826283; PIDN:AA898442.1;
C/Genetics:
A/Map position: REV405287-404964
C/Superfamily: Uncharacterized conserved protein

Query Match 73.5%; Score 36; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YALFPYT 9
Db 60 YVIFPYT 66

RESULT 4

S62520

hypothetical protein SPAC8A4.04c - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe
C/Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Jan-2000
C/Accession: T39126; S62520
R/Lye, G.; Church, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z21830
A/Accession: T39126
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-177 <LY2>
A/Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91514.1; PID:e207901; PID:g132603
C/Genetics:
A/Genes: SPAC8A4.04c
A/Map position: 1

Query Match 73.5%; Score 36; DB 2; Length 177;
Best Local Similarity 66.7%; Pred. No. 8.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 163 LOYAVVNYT 171

RESULT 5

PH1062

Ig light chain V region (clone 202.105) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1062
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1062
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-98 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]P1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 35; DB 2; Length 98;
Best Local Similarity 77.8%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 89 LOYASSPYT 97

RESULT 6

C28840

Ig kappa chain V region (HP22) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000
C/Accession: C28840; J25114
R/Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A/Title: The idiotypic network and the internal image: possible regulation of a germ-line
A/Reference number: A91028; MUID:86136012; PMID:3937730
A/Accession: C28840
A/Molecule type: mRNA
A/Residues: 1-101 <OLL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;10-84/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 35; DB 2; Length 101;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 83 LOYASSPYT 91

RESULT 7

B28840

Ig kappa chain V region (HP27) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000
C/Accession: B28840; I25114
R/Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A/Title: The idiotypic network and the internal image: possible regulation of a germ-line
A/Reference number: A91028; MUID:86136012; PMID:3937730
A/Accession: B28840
A/Molecule type: mRNA
A/Residues: 1-101 <OLL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;10-84/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 35; DB 2; Length 101;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 83 LOYASSPYT 91

RESULT 8

PL0262

Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: P10262
R/Shlomchik, M.; Macecell, M.; Shan, H.; Radic, M.Z.; Pisecky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: P10231; MUID:90111618; PMID:2104919
A/Accession: P10262
A/Molecule type: mRNA
A/Residues: 1-106 <SHL>
C/Superfamily: immunoglobulin V region, immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F.1-23/Region: framework 1
F.16-90/Domain: immunoglobulin homology <IMM>
F.124-34/Region: complementarity-determining 1
F.135-49/Region: framework 2
F.150-56/Region: complementarity-determining 2
F.157-88/Region: framework 3
F.189-97/Region: complementarity-determining 3
F.198-106/Region: framework 4

Query Match 71.4%; Score 35; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 89 LOYASFPWT 97

RESULT 9
KIHWE
Ig kappa chain V-I region (WEA) - human
C/Species: Homo sapiens (man)
C/Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C/Accession: A01876
R/Gont, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A/Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) w
A/Reference number: A93964; MUID:83237307; PMID:6410398
A/Accession: A01876
A/Molecule type: protein
A/Residues: 1-108 <GON>
A/Cross-references: UNIPROT:P01610
C/Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated ga
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer
F.16-90/Domain: immunoglobulin homology <IMM>
F.123-88/Disulfide bonds: #status predicted

Query Match 71.4%; Score 35; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 89 LOYSSFPWT 97

RESULT 10
C71857
Probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: C71857
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mille, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 1
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: C71857
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-398 <ARN>
A/Cross-references: UNIPROT:Q9ZXR7; GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD0660
A/Experimental source: strain J99
C/Genetics:
A/Gene: jhp1032

Query Match 69.4%; Score 34; DB 2; Length 398;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
Db 212 IEXCVFPY 219

RESULT 11
T50279
Hypothetical serine/threonin repeat protein [imported] - fission yeast (Schizosaccharomy
C/Species: Schizosaccharomyces pombe
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: T50279
R/Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A/Reference number: Z25053
A/Accession: T50279
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-416 <ZIM>
A/Cross-references: UNIPROT:Q9P329; EMBL:AL137130; PIDN:CAB69629.1; GSPDB:GN00066; SPDB:6
C/Genetics:
A/Experimental source: strain 972h(-); cosmid c977
A/Gene: SPDB:SPAC977.07c
A/Map position: 1

Query Match 69.4%; Score 34; DB 2; Length 416;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
Db 195 LEYAVDYDT 203

RESULT 12
A64658
LPS biosynthesis protein - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C/Accession: A64658
R/Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khajak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: A64658
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-431 <TOM>
A/Cross-references: UNIPROT:O25733; GB:AE000617; GB:AE000511; NID:g2314256; PIDN:AAD08151

Query Match 69.4%; Score 34; DB 2; Length 431;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYAIIPPY 8
 :|:|:|
 Db 212 IEYCVFPY 219

RESULT 13

H84019
 hypothetical protein BH2960 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: H84019
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A/Reference number: A83650; PMID:11058132
 A/Accession: H84019
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-97 <STO>
 A/Cross-references: UNIPROT:Q9K8P3; GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BAB066
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH2960

Query Match 67.3%; Score 33; DB 2; Length 97;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYAIIPPY 8
 :|:|:|
 Db 37 LEYAIFFAY 44

RESULT 14

F83707
 hypothetical protein BH0462 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: F83707
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A/Reference number: A83650; PMID:11058132
 A/Accession: F83707
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-107 <STO>
 A/Cross-references: UNIPROT:Q9KFL7; GB:AP001508; GB:BA000004; NID:G10172890; PIDN:BAB041
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH0462

Query Match 67.3%; Score 33; DB 2; Length 107;
 Best Local Similarity 83.3%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAIIPPY 8
 :|:|:|
 Db 48 YALFPY 53

RESULT 15

S42466
 Ig kappa chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S42466
 R/Shiyanov, P.A.; Bespalov, I.A.; Terletsckaya, H.N.; Deyev, S.M.
 submitted to the EMBL Data Library, March 1994
 A/Reference number: S42466
 A/Accession: S42466
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-117 <SH1>
 A/Cross-references: EMBL:X78108; NID:G460824; PIDN:CAA54998.1; PID:G460825
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/26-100/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 33; DB 2; Length 117;
 Best Local Similarity 62.5%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYAIIPPY 9
 :|:|:|
 Db 100 QYSSYPY 107

Search completed: April 4, 2005, 15:58:04
 Job time : 5.2492 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 15.2109 Seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_222_230
Perfect score: 49
Sequence: 1 LGYAFPPY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 41 | 83.7 | 173 | 2 | 096YG9 sulfolobus |
| 2 | 40 | 81.6 | 417 | 2 | 072ZM4 eleutheroda |
| 3 | 39 | 79.6 | 135 | 2 | 0654Q7 coryza sativ |
| 4 | 39 | 79.6 | 450 | 2 | 029288 archaeoglob |
| 5 | 38 | 77.6 | 628 | 2 | 07RXK3 coryxk3 neurospora |
| 6 | 38 | 77.6 | 654 | 2 | 07S014 neurospora |
| 7 | 36 | 73.5 | 107 | 1 | Y453 METUA |
| 8 | 36 | 73.5 | 274 | 2 | 06NCK4 methanococc |
| 9 | 36 | 73.5 | 276 | 2 | 07PEU2 fusobacteri |
| 10 | 36 | 73.5 | 300 | 2 | 087HF9 vibrio para |
| 11 | 36 | 73.5 | 301 | 2 | 06LENO photobacter |
| 12 | 36 | 73.5 | 454 | 2 | 098UD2 xenopus bor |
| 13 | 36 | 73.5 | 455 | 1 | VEGT XENTLA |
| 14 | 36 | 73.5 | 455 | 2 | 013161 xenopus lae |
| 15 | 36 | 73.5 | 455 | 2 | 098UD1 xenopus lae |
| 16 | 36 | 73.5 | 1366 | 2 | 086AM2 dictyosteli |
| 17 | 35 | 71.4 | 108 | 1 | KVLR HUMAN |
| 18 | 35 | 71.4 | 127 | 2 | 092559 mus musculu |
| 19 | 35 | 71.4 | 173 | 2 | 07WTIS escherichia |
| 20 | 35 | 71.4 | 233 | 2 | 0859G6 pseudomonas |
| 21 | 35 | 71.4 | 314 | 2 | 07SEL3 neurospora |
| 22 | 35 | 71.4 | 329 | 2 | 06LZJ1 picophilus |
| 23 | 35 | 71.4 | 347 | 2 | 08PR41 methanocarc |
| 24 | 35 | 71.4 | 361 | 2 | 086A83 dictyosteli |
| 25 | 35 | 71.4 | 442 | 2 | 07Q608 anopheles g |
| 26 | 35 | 71.4 | 553 | 2 | 024194 drosophila |
| 27 | 35 | 71.4 | 565 | 2 | 09VIC3 drosophila |
| 28 | 35 | 71.4 | 693 | 2 | 095TH0 drosophila |
| 29 | 35 | 71.4 | 693 | 2 | 09VIX4 drosophila |
| 30 | 35 | 71.4 | 703 | 2 | 08SXA1 drosophila |
| 31 | 35 | 71.4 | 745 | 2 | 0747M0 geobacter s |

| | | | | | |
|----|----|------|------|---|-----------------------|
| 32 | 35 | 71.4 | 879 | 2 | 076858 drosophila |
| 33 | 35 | 71.4 | 879 | 2 | 09YDC6 drosophila |
| 34 | 35 | 71.4 | 945 | 2 | 07R3B3 giardia lam |
| 35 | 35 | 71.4 | 2396 | 2 | 07U132 rhodospirillum |
| 36 | 34 | 69.4 | 325 | 2 | 06LQ11 photobacter |
| 37 | 34 | 69.4 | 348 | 2 | 06WN37 eleutheroda |
| 38 | 34 | 69.4 | 398 | 2 | 09ZKA7 heliobacter |
| 39 | 34 | 69.4 | 416 | 2 | 09P329 schizosacch |
| 40 | 34 | 69.4 | 425 | 2 | 082VZ6 nitrosomonas |
| 41 | 34 | 69.4 | 431 | 2 | 025733 heliobacter |
| 42 | 34 | 69.4 | 779 | 2 | 07S947 neurospora |
| 43 | 34 | 69.4 | 870 | 2 | 08ISP3 plasmodium |
| 44 | 33 | 67.3 | 79 | 2 | 08GR38 enterococcu |
| 45 | 33 | 67.3 | 97 | 2 | 09K8P3 bacillus ha |

ALIGNMENTS

```
RESULT 1
ID 096YG9 PRELIMINARY; PRT; 173 AA.
AC 096YG9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein STR2202.
GN OrderedlocusNames=STR2202;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus;
NCBI_Taxid=11955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / ?
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kuehida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AF000989; BAB67308.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 173 AA; 19383 MW; 14F1F8ADP102BCD CRC64;

Query Match 83.7%; Score 41; DB 2; Length 173;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGYAFPPY 9
Db 120 VRYAVFPYT 128

RESULT 2
ID 072ZM4 PRELIMINARY; PRT; 417 AA.
AC 072ZM4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Vegt.
OS Eleutherodactylus coqui (Puerto Rican coqui).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobiinae; Eleutherodactylus.
NCBI_Taxid=57060;
RN [1]
RP SEQUENCE FROM N.A.
```

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RA Beckham Y.M., Nath K., Elinson R.P.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY51031; AAP20869.1; -.
DR HSSP; O15119; 1H6F.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006967; P53 like DNA_bnd.
DR InterPro; IPR001699; TF_T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS50252; TBOX_3; 1.
SQ SEQUENCE 417 AA; 47815 MW; 23CB46DB5E5B5C09 CRC64;

Query Match
Best Local Similarity 81.6%; Score 39; DB 2; Length 417;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYAFPT 9
Db 408 QYSLFPT 415

RESULT 3
065407 PRELIMINARY; PRT; 135 AA.
AC 065407;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Hypothetical protein OSUNBA0091G06.4.
GN Name=OSUNBA0091G06.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSUNBA0091G06."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004651; BAD45710.1; -.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14500 MW; C2A82C97536D420B CRC64;

Query Match
Best Local Similarity 79.6%; Score 39; DB 2; Length 135;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPT 9
Db 117 YAVFPT 123

RESULT 4
029288 PRELIMINARY; PRT; 450 AA.
AC 029288;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bile acid-inducible operon protein F (Balf-2).
OS OrderedocusNames=AF0974;
OC Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gilm M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Retch C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Uiterback T.R., Cotton M.D., Spriggs T., Artach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Moese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE001037; AAB90269.1; -.
DR PIR; F69371; F69371.
DR HSSP; P77407; 1PQY.
DR TIGR; AF0974; -.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CA1B_BAIF.
DR Pfam; PF02515; COA_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 450 AA; 51287 MW; 968FC97249CFA8B4 CRC64;

Query Match
Best Local Similarity 79.6%; Score 39; DB 2; Length 450;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YAFPT 9
Db 275 YAVFPT 281

RESULT 5
07RXK3 PRELIMINARY; PRT; 628 AA.
AC 07RXK3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU03976.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selzer E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gagne S.,
RA Kamai M., Kamysseis M., Mauceli E., Bielek C., Rudd S., Frisman D.,
RA Krysstova S., Rasmussen C., Metzger R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Piamann M., Selter S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manthaupt G., Ebbole D.U., Freitag M.,
RA Paulsen I., Sachs W.S., Lander E.S., Nussbaum C., Birren B.;
RT "The genome sequence of the filamentous fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100743; EAA27327.1; -.
DR HSSP; P22303; 1B41.

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DR GO:0003824; F: catalytic activity; IEA.
DR InterPro: IPR002018; CarbohydraseB.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF00135; Coesterase; 1.
KW Hypothetical protein.
SQ SEQUENCE 628 AA; 68076 MW; 0F363A75105971F3 CRC64;

Query Match
Best Local Similarity 77.6%; Score 38; DB 2; Length 628;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
   :|:|:|:|
DB 460 MOYSVFPY 467

RESULT 6
Q78014 PRELIMINARY; PRT; 654 AA.
ID Q78014
AC Q78014
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU10022.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR7A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Erdiczi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Maehurne M.,
RA Seiltnmukoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schlite U.,
RA Korte G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseila M., Mauceli E., Bleike C., Rudd S., Fishman D.,
RA Kryzocova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Marino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desguza C.C., Glas L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABX01000496; EAA28821.1; -.
DR HSBP; P22303; 1P8U.
DR GO:0003824; F: catalytic activity; IEA.
DR InterPro: IPR002018; CarbohydraseB.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF00135; Coesterase; 1.
KW Hypothetical protein.
SQ SEQUENCE 654 AA; 70515 MW; 99F744A903948390 CRC64;

Query Match
Best Local Similarity 77.6%; Score 38; DB 2; Length 654;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
   :|:|:|:|
DB 466 MOYSVFPY 493

RESULT 7
Y453 METJA STANDARD; PRT; 107 AA.
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AC Q57895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MJ0453.
GN Ordered locus names=MJ0453;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bull C.V., White O., Olsen G.V., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Huret M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Frazer C.M., Smith H.O., Woebe C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RL Science 273:1058-1073 (1996).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U67496; AAB98442.1; -.
DR PIR; E64356; E64356.
DR TIGR; MJ0453; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 107 AA; 12603 MW; 4B3723628AEF3F8F CRC64;

Query Match
Best Local Similarity 73.5%; Score 36; DB 1; Length 107;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YALFPYT 9
   |||||
DB 60 YVIFPYT 66

RESULT 8
Q6NCK4 PRELIMINARY; PRT; 274 AA.
ID Q6NCK4
AC Q6NCK4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative ATP-binding protein of ABC transporter.
GN Ordered locus names=RPA0468;
OS Rhodospseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Belletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobet C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile
RA photosynthetic bacterium Rhodospseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
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CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL: BX572594; CAE25912.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transporter activity; IEA.
DR InterPro: IPR000515; BPD transp.
DR Pfam: PF00528; BPD transp. 1; 1.
DR PROSITE: PS50928; ABC_TML_1.
DR ATP-binding, Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 274 AA; 29247 MW; 1D1088FDD101A759 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 274;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYALFPY 8
DB 102 LEXSLFPY 109

RESULT 9
Q7P6U2 PRELIMINARY; PRT; 276 AA.
AC Q7P6U2;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=FN1599;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
CC NCB1_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Karabeli V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Watkins T.,
RA Haselkorn R., Overbeek R., Kyriides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABP0100027; EAA24518.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 276 AA; 32878 MW; 66E734344433381 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 276;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYALFPYT 9
DB 66 IYLLIFPYT 74

RESULT 10
Q87HF9 PRELIMINARY; PRT; 300 AA.
AC Q87HF9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transcriptional regulator, LysR family.
GN OrderedLocusNames=VPA1006;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

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OC Vibrionales; Vibrio.
OX NCB1_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749 (2003).
CC -!- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
DR EMBL: AP005087; BAC62349.1; -.
DR GO: GO:0003700; F: transcription factor activity; IEA.
DR GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR subst.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS: PR00039; HTH_LysR.
DR PROSITE: PS50931; HTH_LysR; 1.
DR KW Complete proteome; DNA-binding; Transcription;
DR Transcription regulation.
SQ SEQUENCE 300 AA; 33894 MW; DDA07EAF2EB68601 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YALFPYT 9
DB 269 YAVVPYT 275

RESULT 11
Q6LPN0 PRELIMINARY; PRT; 301 AA.
AC Q6LPN0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical transcriptional regulator, LysR family.
GN Name=V21654; OrderedLocusNames=BBPR2361;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCB1_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR378670; CAG20746.1; -.
DR GO: GO:0003700; F: transcription factor activity; IEA.
DR GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR subst.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PROSITE: PS50931; HTH_LysR; 1.
DR KW Complete proteome.
SQ SEQUENCE 301 AA; 33862 MW; 3A6D90E214EDA8B0 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 301;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY      3 YAIPTPT 9
      ||::|||
Db      270 YAIPTPT 276

RESULT 12
O98UD2
ID      098UD2      PRELIMINARY;      PRT;      454 AA.
AC      098UD2
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Vegt.
GN      Name=Vegt;
OS      Xenopus borealis (Kenyan clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCB1_TaxID=8354;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bubuneko M., Vempati U.D., King M.L.;
RL      Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF180351; AAK00596.1; -.
DR      HSBP; O15119; IH6F.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR008967; P53 like DNA_bnd.
DR      InterPro; IPR001699; TP_T-box.
DR      Pfam; PF00907; T-box; 1.
DR      PRINTS; PR00937; TBOX.
DR      SMART; SM00425; TBOX; 1.
DR      PROSITE; PS01283; TBOX_1; 1.
DR      PROSITE; PS01264; TBOX_2; 1.
DR      PROSITE; PS50252; TBOX_3; 1.
SO      SEQUENCE 454 AA; 51855 MW; 4623D860475AD6AC CRC64;

Query Match      73.5%; Score 36; DB 2; Length 454;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      2 QYAIPTPT 9
      ||::|||
Db      445 QYSLPPTS 452

RESULT 13
VEGT_XENLA      STANDARD;      PRT;      455 AA.
ID      VEGT_XENLA      P87377; P79930; P87386;
AC      P87377; P79930; P87386;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      T-box protein VEGT (T-box protein BRAT) (T-box protein antipodean).
GN      Name=VEGT; Synonym=APOD, BRAT;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCB1_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Hord M.E., Thomsen G.H.;
RL      Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      TISSUE=Oocyte;
RX      MEDLINE=97164724; PubMed=9012531;
RA      Zhang J., King M.L.;
RT      "Xenopus Vegt RNA is localized to the vegetal cortex during oogenesis
      and encodes a novel T-box transcription factor involved in mesodermal

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RT      patterning.";
RL      Development 122:4119-4129 (1996).
RN      [3]
RP      REVISIONS TO 209 AND 396-455.
RN      [3]
RA      Zhang J., King M.L.;
RL      Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=97164730; PubMed=9012537;
RA      Sternard F., Carnac G., Gurdon J.B.;
RT      "The Xenopus T-box gene, Antipodean, encodes a vegetally localised
      maternal mRNA and can trigger mesoderm formation.";
RL      Development 122:4179-4188 (1996).
CC      -1- FUNCTION: Transcription factor involved in mesodermal patterning.
      Appears to pattern mesoderm along the dorsoventral and posterior
      axis. It activates WNT-8, EOMES and brachyury expression.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- TISSUE SPECIFICITY: Expressed both maternally and zygotically.
      Maternally localized to the egg vegetal hemisphere, and in the
      developing embryo, in the posterior paraxial mesoderm and ventral
      blastopore.
CC      -1- DEVELOPMENTAL STAGE: Maternally expressed from early oogenesis.
      Zygotic expression occurs from late blastula and reaches maximum
      levels during gastrulation (stages 10.5-12). Levels decline at the
      time of blastopore closure (stage 13).
CC      -1- INDUCTION: By TGF-beta family members.
CC      -1- SIMILARITY: Contains 1 T-box domain.
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DR      EMBL; U89707; AAB49478.1; -.
DR      EMBL; U59483; AAB93301.1; -.
DR      EMBL; X59905; CAA68179.1; -.
DR      HSBP; O15119; IH6F.
DR      InterPro; IPR008967; P53 like DNA_bnd.
DR      InterPro; IPR001699; TP_T-box.
DR      Pfam; PF00907; T-box; 1.
DR      PRINTS; PR00937; TBOX.
DR      PROSITE; PS01283; TBOX_1; 1.
DR      PROSITE; PS01264; TBOX_2; 1.
DR      PROSITE; PS50252; TBOX_3; 1.
KM      Developmental protein; DNA-binding; Nuclear protein;
      Transcription regulation.
FT      DNA_BIND 57 230
FT      CONFLICT 1 25
FT      REF 3)
FT      SEQUENCE 244 244 H -> L (in Ref. 2 and 3).
SQ      SEQUENCE 455 AA; 51795 MW; 9DD12CD704F2AE07 CRC64;

Query Match      73.5%; Score 36; DB 1; Length 455;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      2 QYAIPTPT 9
      ||::|||
Db      446 QYSLPPTS 453

RESULT 14
O13161
ID      O13161      PRELIMINARY;      PRT;      455 AA.
AC      O13161
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DT      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT      25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE      T-box protein (Xombi protein).

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GN Name=Xombi;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97164713; PubMed=9012520;
 RA Lustig K.D., Kroll K.L., Sun E.E., Kirschner M.W.;
 RT "Expression cloning of a Xenopus T-related gene (Xombi) involved in
 mesodermal patterning and blastopore lip formation.";
 RL Development 122:4001-4012 (1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Miliutin S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz D., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX TISSUE=Oocytes;
 RL MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX TISSUE=Oocytes;
 RA Klein S., Strausberg R.,
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; S83518; AAB50917.1; -.
 DR EMBL; BC070708; AAH70708.1; -.
 DR HSSP; O15119; 1H6F.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR001699; TF_T-box.
 DR Pfam; PF00907; T-box; 1.
 DR PRINTS; PR00937; TBOX.
 DR SMART; SM00425; TBOX; 1.
 DR PROSITE; PS01283; TBOX_1; 1.
 DR PROSITE; PS01264; TBOX_2; 1.
 DR PROSITE; PS50252; TBOX_3; 1.
 SO SEQUENCE 455 AA; 51963 MW; 2B9C8FBCCD7B37D CRC64;

DB 446 QXSLPFS 453

RESULT 15
 ID 098UD1 PRELIMINARY; PRT; 455 AA.
 AC 098UD1;
 DT 01-JUN-2001 (TRIMBLREL 17, Created)
 DT 01-JUN-2001 (TRIMBLREL 17, Last sequence update)
 DT 01-MAR-2004 (TRIMBLREL 26, Last annotation update)
 DE VegT.
 GN Name=VegT;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bubnenko M., Vempati U.D., King M.L.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF180352; AAK00597.1; -.
 DR HSSP; O15119; 1H6F.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR001699; TF_T-box.
 DR Pfam; PF00907; T-box; 1.
 DR PRINTS; PR00937; TBOX.
 DR SMART; SM00425; TBOX; 1.
 DR PROSITE; PS01283; TBOX_1; 1.
 DR PROSITE; PS01264; TBOX_2; 1.
 DR PROSITE; PS50252; TBOX_3; 1.
 SO SEQUENCE 455 AA; 51890 MW; 0D2502AF91CBA2B0 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 455;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYALPPT 9
 DB 446 QXSLPFS 453

Search completed: April 4, 2005, 15:56:19
 Job time : 20.2109 secs

OY 2 QYALPPT 9
 ||::|||:

Query Match 73.5%; Score 36; DB 2; Length 455;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 9.98403 seconds

(without alignments)
193.690 Million cell updates/secTitle: US-09-887-853-6_COPY_31_35
Perfect score: 30
Sequence: 1 NYGMN 5Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16dec04:*

- 1: geneeqp19808:*
- 2: geneeqp19908:*
- 3: geneeqp20008:*
- 4: geneeqp20018:*
- 5: geneeqp20028:*
- 6: geneeqp20038:*
- 7: geneeqp20038:*
- 8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1 | 30 | 100.0 | 5 | 2 | AAR85496 |
| 2 | 30 | 100.0 | 5 | 2 | AAW24504 |
| 3 | 30 | 100.0 | 5 | 3 | AAV32223 |
| 4 | 30 | 100.0 | 5 | 3 | AAU80973 |
| 5 | 30 | 100.0 | 5 | 7 | ABR61517 |
| 6 | 30 | 100.0 | 5 | 8 | ADG34365 |
| 7 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 8 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 9 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 10 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 11 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 12 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 13 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 14 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 15 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 16 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 17 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 18 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 19 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 20 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 21 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 22 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 23 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 24 | 30 | 100.0 | 5 | 8 | ADL23057 |
| 25 | 30 | 100.0 | 5 | 8 | ADL23057 |

| | | | | | | | |
|----|----|-------|-----|---|----------|----------|-----------|
| 26 | 30 | 100.0 | 92 | 2 | AAW24529 | AAW24529 | Anti-Fact |
| 27 | 30 | 100.0 | 92 | 2 | AAU80997 | AAU80997 | Human ant |
| 28 | 30 | 100.0 | 112 | 2 | AAW24521 | AAW24521 | Anti-Fact |
| 29 | 30 | 100.0 | 112 | 5 | AAU80980 | AAU80980 | Human ant |
| 30 | 30 | 100.0 | 115 | 3 | AAV90823 | AAV90823 | 520C9 hyb |
| 31 | 30 | 100.0 | 115 | 4 | AAW84740 | AAW84740 | Variable |
| 32 | 30 | 100.0 | 116 | 4 | AAW84739 | AAW84739 | Variable |
| 33 | 30 | 100.0 | 116 | 5 | AAE27830 | AAE27830 | Mouse KS |
| 34 | 30 | 100.0 | 116 | 5 | AAE27839 | AAE27839 | Mouse KS |
| 35 | 30 | 100.0 | 116 | 5 | AAE27837 | AAE27837 | Mouse KS |
| 36 | 30 | 100.0 | 116 | 5 | AAE27825 | AAE27825 | Mouse KS |
| 37 | 30 | 100.0 | 116 | 5 | AAE27826 | AAE27826 | Mouse KS |
| 38 | 30 | 100.0 | 116 | 5 | AAE27828 | AAE27828 | Mouse KS |
| 39 | 30 | 100.0 | 116 | 5 | AAE27832 | AAE27832 | Mouse KS |
| 40 | 30 | 100.0 | 116 | 5 | AAE27834 | AAE27834 | Mouse KS |
| 41 | 30 | 100.0 | 116 | 5 | ADG67541 | ADG67541 | KS antibo |
| 42 | 30 | 100.0 | 116 | 5 | ADG67537 | ADG67537 | KS antibo |
| 43 | 30 | 100.0 | 116 | 5 | ADG67543 | ADG67543 | KS antibo |
| 44 | 30 | 100.0 | 116 | 5 | ADG67531 | ADG67531 | KS antibo |
| 45 | 30 | 100.0 | 116 | 5 | ADG67533 | ADG67533 | KS antibo |

ALIGNMENTS

RESULT 1
AAR85496 standard; peptide; 5 AA.
ID AAR85496
XX
AC AAR85496;
XX
DT 16-MAR-1996 (first entry)
XX
DE SCFV(FRP)5 CDR1H.
XX
KW Single chain antibody; scFv; antibody engineering; antitumor;
KW tumour antigen binding; cytotoxic T-lymphocyte; cell targeting;
KW monoclonal antibody; erB-2; cancer; adoptive immunotherapy;
KW complementarity determining region; CDR.
XX
OS Synthetic.
XX
PN WO9530014-A1.
XX
PD 09-NOV-1995.
XX
PF 20-APR-1995; 95WO-EP001494.
XX
PR 02-MAY-1994; 94EP-00810244.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Groner B, Moritz D;
XX
DR WPI, 1995-393085/50.
XX
PT New bifunctional proteins for use in killing tumour cells - contg. a
PT tumour antigen binding domain, a hinge region and a zeta chain derived
PT from a T-cell antigen receptor.
XX
PS Disclosure; Page 6; 46pp; English.
XX
XX Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H
CC (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components of
CC the heavy chain variable region and light chain variable region,
CC respectively, of single chain antibody scFv(FRP)5 (AAR85494). The CDRs
CC are derived from mouse monoclonal antibody FRP5 (EGACC 90112115). The
CC scFv is specific for the extracellular domain of erbB-2, and is used as
CC the tumour antigen binding domain of a bifunctional protein that is
CC expressed in cytotoxic T-lymphocytes (CTLs), allowing adoptive
CC immunotherapy of cancer
XX
SQ Sequence 5 AA:

Query Match 100.0%; Score 30; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
 |||||
 DB 1 NYGMN 5

RESULT 2
 AAM24504
 ID AAM24504 standard; peptide; 5 AA.

XX AAM24504;

DT 26-DEC-1997 (first entry)

DE Mouse anti-human Factor IX antibody BC2 heavy chain CDR1.

KM Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;

KW humanised antibody; antibody engineering; heavy chain; CDR;

KM complementarity determining region; myocardial infarction; angina;

KW atrial fibrillation; stroke; kidney damage; pulmonary embolism;

KM deep vein thrombosis; coronary angioplasty; pulmonary embolism;

KW disseminated intravascular coagulation; artificial organ; sepsis; shunt;

KM prostheses.

XX Mus musculus.

OS Mus musculus.

XX MO9726010-A1.

XX 24-JUL-1997.

PF 17-JAN-1997; 97MO-US000759.

XX 17-JAN-1996; 96US-0010108P.

PR 24-OCT-1996; 96US-0029119P.

PI (SMIR) SMITHKLINE BEECHAM CORP.

PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PI Blackburn MN, Church WR, Feuerstein GZ, Grose MS, Nichols AJ;

DR Padlan EA, Patel AH, Sylvester DR;

XX WPI; 1997-385117/35.

XX Claim 21; Page 65; 150pp; English.

CC This peptide comprises complementarity determining region 1 (CDR1) of the
 CC heavy chain variable region (VH) of mouse anti-human Factor IX monoclonal
 CC antibody BC2 (see also AAM24519). Claimed humanised antibodies (see
 CC AAM24510-18) contain CDRs (see AAM24504-09) of BC2 VH and VL inserted
 CC into framework regions of selected human antibody sequences. They have
 CC self-limiting neutralising activity, and are useful as anticoagulant
 CC agents in treatment of thrombosis associated with myocardial infarct,
 CC unstable angina, atrial fibrillation, stroke, renal damage, pulmonary
 CC embolism, deep vein thrombosis, percutaneous transluminal coronary
 CC angioplasty, disseminated intravascular coagulation, sepsis, or
 CC artificial organs, shunts or prostheses (claimed). Also claimed are
 CC chimeric antibodies, as well as Fab and Fab'2 fragments. The claimed
 CC antibodies do not cause uncontrolled bleeding (contrast heparin and
 CC warfarin) since they provide only partial inhibition of coagulation

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
 |||||
 DB 1 NYGMN 5

RESULT 3
 AAY32223
 ID AAY32223 standard; peptide; 5 AA.

XX AAY32223;

DT 15-FEB-2000 (first entry)

DE G-CSF agonist antibody mAb163-93 heavy chain variable region CDR1.

XX Granulocyte colony stimulating factor receptor; G-CSF; mouse;

KW monoclonal antibody; agonist; screening; neutropenia; therapy;

KM complementarity determining region; CDR; mAb163-93.

XX Mus musculus.

OS WO9955735-A1.

PN 04-NOV-1999.

PD 30-APR-1999; 99MO-US009466.

PF 30-APR-1998; 98US-0083575P.

PR (TANO-) TANOX INC.

PI Ni B, Sun BNC, Sun CRY;

DR WPI; 2000-052805/04.

XX Treatment of neutropenia by stimulating proliferation of neutrophilic

PT cell lineage progenitors.

XX Claim 13; Page 30; 64pp; English.

CC The present sequence represents complementarity determining region 1
 CC (CDR1) of the heavy chain variable region of murine monoclonal antibody
 CC mAb163-93. This antibody is an example of an agonist molecule that
 CC specifically binds to or interacts with human granulocyte colony
 CC stimulating factor (G-CSF) receptor to stimulate cell proliferation and
 CC differentiation, especially by dimerising with the receptor or activating
 CC phosphorylation of kinases associated with the receptor. Agonist
 CC antibodies can be used to stimulate proliferation of G-CSF-dependent
 CC cells, e.g. to differentiate leading to a repopulation of neutrophilic
 CC granulocyte lineage cells, especially to treat neutropenia (claimed).
 CC They can also be used to detect human G-CSF receptor immunologically

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
 |||||
 DB 1 NYGMN 5

RESULT 4
 AAU80973
 ID AAU80973 standard; peptide; 5 AA.

XX AAU80973;

DT 09-APR-2002 (first entry)

DE Murine BC2 heavy chain variable region CDR1.

KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
KW thrombolytic agent; anti-factor IX antibody; plasminogen activator;
KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KW vasotrophic; cardiac; anti-respiratory syncytial virus;
KW heavy chain variable region; light chain variable region.
OS Mus sp.
XX WO200187339-A1.
PN 22-NOV-2001.
XX 05-OCT-2000; 2000WO-US027438.
PF 15-MAY-2000; 2000US-00571434.
PR (SMIK) SMITHKLINE BEECHAM CORP.
XX Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
PI WPI; 2002-082944/11.
DR WPI; 2002-082944/11.
XX Treating post-thromboembolic induced ischemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator.
XX Example 5; Page 95; 163pp; English.
XX The invention relates to a method for treating an animal post-
CC thromboembolic induced ischemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischaemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating post-thromboembolic
CC -induced ischaemia, for preventing thromboembolic stroke in an animal,
CC and for reducing a required dose of a thrombolytic agent. Sequences
CC AAU80972-AAU81004 represent antibodies and vector polypeptides used in
CC the method of the invention
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 30; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYGMN 5
DB 1 NYGMN 5
RESULT 5
ABR61517
ID ABR61517 standard; peptide; 5 AA.
XX ABR61517;
AC ABR61517;
XX 15-JAN-2004 (first entry)
DT 15-JAN-2004 (first entry)
XX Humanised RS7 antibody heavy chain variable region CDR1 fragment.
DE Humanised RS7 antibody heavy chain variable region CDR1 fragment.
XX EGP-1; glycoprotein; cytosolic; antigen binding protein; cancer;
KW RS7 antibody; complementarily determining region; CDR.
XX Homo sapiens.
OS WO2003074566-A2.
XX 12-SEP-2003.
PD 03-MAR-2003; 2003WO-GB000885.
PF 01-MAR-2002; 2002US-0360229P.
PR 01-MAR-2002; 2002US-0360229P.
XX

PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX Govindan S, Qu Z, Hansen HJ, Goldenberg DM;
PI WPI; 2003-767380/72.
XX RPI; 2003-767380/72.
XX Monovalent and multivalent humanized RS7 antigen binding proteins useful
PT in the diagnosis and therapy of cancer.
PT Claim 6; Page 65; 97pp; English.
XX The invention relates to an antibody (Ab) or fragment that binds to an
CC EGP-1 glycoprotein. The methods are useful for delivering a diagnostic or
CC therapeutic composition, diagnosing or treating cancer, treating a
CC malignancy, and treating a cancer cell. A therapeutic conjugate or
CC diagnostic conjugate comprising EGP-1 Mab, a fragment of an antibody
CC fusion protein or fragment is used for the diagnosis or treatment of a
CC malignancy when bound to at least one therapeutic agent. The diagnostic/
CC therapeutic agent or a combination of both comprising at least one Ab are
CC used for targeting an EGP-1 target antigen on a cell. The cancers are
CC lung, ovarian, prostate, colon, stomach, bladder and breast cancer. Naked
CC anti-EGP-1 Mab or fragment is used for the treatment of cancer. The
CC invention provides multivalent, monospecific binding proteins that are
CC useful in a direct targeting system and for production of multivalent,
CC multispecific binding proteins that are useful in an affinity enhancement
CC system. The present sequence represents a humanised anti-EGP-1 antibody
CC heavy chain variable region CDR1 fragment
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 30; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYGMN 5
DB 1 NYGMN 5
RESULT 6
ADG34365
ID ADG34365 standard; peptide; 5 AA.
XX ADG34365;
AC ADG34365;
XX 26-FEB-2004 (first entry)
DT 26-FEB-2004 (first entry)
XX Humanised mouse BAT-1 antibody-derived HC variable region seqID9.
DE Humanised mouse BAT-1 antibody-derived HC variable region seqID9.
XX humanised monoclonal antibody; complementarily determining region; CDR;
KW murine monoclonal antibody BAT-1; mBAT-1; framework region; PR;
KW acceptor human immunoglobulin; anti-tumour; immunogenic; cytostatic;
KW anti-HIV; immunotherapy; cancer; HIV infection; autoimmune disorder;
KW immune deficiency; mouse; murine; heavy chain variable region.
XX Mus sp.
OS WO2003099196-A2.
XX 04-DEC-2003.
PD 22-MAY-2003; 2003WO-IL000425.
PF 23-MAY-2002; 2002IL-00149820.
PR (CURE-) CURE TECH LTD.
XX (MORR-) MOR RES APPL LTD.
PA Hardy B, Jones ST, Klapper L;
PI WPI; 2004-035027/03.
DR WPI; 2004-035027/03.
XX

CC sequence corresponds to the complementarity determining region 1 (CDR1)
 CC of the heavy chain of the antibody of the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
 |||||
 DB 1 NYGMN 5

RESULT 9

ADS88789 ADS88789 standard; peptide; 5 AA.

AC ADS88789;

DT 16-DEC-2004 (first entry)

DE Heavy chain CDR H1 of an anti-MAG antibody.

XX oligodendrocyte; stroke; neurological disease;
 XX myelin-associated glycoprotein; MAG; anti-MAG antibody;
 XX Alzheimer's disease; multiple sclerosis;
 XX chain complementarity determining region; CDR.

OS Unidentified.

PN WO2004083363-A2.

PD 30-SEP-2004.

PF 02-FEB-2004; 2004WO-EP001016.

PR 19-MAR-2003; 2003GB-00006309.

PA (GLAX) GLAXO GROUP LTD.

PI Vinson M, Irving EA;

DR WPI; 2004-691029/67.

XX Promoting oligodendrocyte survival in humans with neurological diseases,
 PT such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
 PT anti-myelin-associated glycoprotein (MAG) antibody.

PS Claim 6; SEQ ID NO 4; 45bp; English.

XX The specification describes a method for promoting oligodendrocyte
 CC survival in a human suffering or at risk of developing stroke or another
 CC neurological disease. The method comprises administering to the human an
 CC anti-myelin-associated glycoprotein (MAG) antibody or its functional
 CC fragment. The anti-MAG antibody or its functional fragment is useful in
 CC the manufacture of a medicament for the promotion of oligodendrocyte
 CC survival in a human suffering from or at risk of developing stroke or
 CC another neurological disease. They can also be used in treating
 CC neurological diseases, such as Alzheimer's disease, multiple sclerosis
 CC and/or stroke, by promoting oligodendrocyte survival. ADS88789-ADS88791
 CC represent the heavy chain complementarity determining regions (CDRs) of
 CC an anti-MAG antibody which can be used in the method of the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
 |||||
 DB 1 NYGMN 5

RESULT 10

AAB99237

XX AAB99237 standard; peptide; 6 AA.

AC AAB99237;

DT 10-SEP-2001 (first entry)

DE Mouse clone 13 CDR1 peptide.

XX Cytostatic; immunostimulation; antibody; H11; tumour; cancer; murine;
 XX antigen-binding fragment; stress protein-peptide complex; SPFC; CDR;
 XX complementarity determining region.

OS Mus sp.

PN WO200140292-A1.

PD 07-JUN-2001.

PF 29-NOV-1999; 99WO-CA001141.

PR 29-NOV-1999; 99WO-CA001141.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Dan M, Entwistle J, Fast D, Kaplan H, Lewis K, Macdonald G;
 PI Malt P;

DR WPI; 2001-356155/37.

XX Antigen-binding fragments specific for stress protein-peptide complexes
 PT (SPFCs) associated with tumors and cancer associated SPFCs, useful for
 PT treating a range of cancers.

PS Example 23; Page 133; 176pp; English.

XX The present invention relates to antigen-binding fragments, which are
 CC specific for stress protein-peptide complexes (SPFCs) associated with
 CC tumours and cancer associated SPFCs. The cancer-specific SPFC complexes
 CC are useful for initiating cancer-specific immunogenic responses against a
 CC variety of cancers: astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural
 CC ectodermal tumour (ENET), chondrosarcoma, osteogenic sarcoma, pancreatic
 CC ductal adenocarcinoma, small and large cell lung adenocarcinomas,
 CC chondroma, angiosarcoma, endothelioma, squamous cell carcinoma,
 CC broncholeovascular carcinoma, epithelial adenocarcinoma, and liver metastases
 CC thereof, lymphangiosarcoma, lymphangioma, endothelioma, hepatoma,
 CC cholangiocarcinoma, synovialoma, mesothelioma, Ewing's tumour,
 CC rhabdomyosarcoma, colon carcinoma, basal cell carcinoma, sweat gland
 CC carcinoma, papillary carcinoma, sebaceous gland carcinoma, papillary
 CC adenocarcinoma, cystadenocarcinoma, medullary carcinoma, bronchogenic
 CC carcinoma, renal cell carcinoma, bile duct carcinoma, choriocarcinoma,
 CC seminoma, embryonal carcinoma, Wilms' tumour, testicular tumour,
 CC craniopharyngioma, pinealoma, hemangioblastoma, acoustic neuroma, kidney
 CC adenocarcinoma, meningioma, neuroblastoma, retinoblastoma, leukaemia,
 CC multiple myeloma, Waldenstrom's macroglobulinaemia, and heavy chain
 CC disease, breast tumours such as ductal and lobular adenocarcinoma,
 CC squamous and adenocarcinomas of the uterine cervix, uterine and ovarian
 CC epithelial carcinomas, prostatic adenocarcinomas, transitional squamous
 CC cell carcinoma of the bladder, B and T cell lymphomas (nodular and
 CC diffuse) plasmacytoma, acute and chronic leukaemias, malignant melanoma,
 CC glioblastoma, colon adenocarcinoma, small cell lung carcinoma, soft
 CC tissue sarcomas, ovarian adenocarcinoma, ovarian adenocarcinoma, bladder
 CC cell carcinoma, prostate adenocarcinoma, larynx carcinoma and
 CC leiomyosarcomas. The present sequence is a complementarity determining
 CC region (CDR) peptide from mouse clone 13, which was used in an example
 CC from the present invention. Mouse clone 13 was derived via mouse scfv
 CC library panning against SPFC H11, for the isolation of binders to the
 CC antigen. Mouse clone 13 was found to show specific binding to SPFC

XX

SQ Sequence 6 AA:

| | | | | |
|-------------------------|--------|--------------------|-----------|-----------|
| Query Match | 100.0% | Score 30; | DB 4; | Length 6; |
| Best Local Similarity | 100.0% | Pred. No. 1.5e+06; | | |
| Matches 5; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|---|-------|---|
| Qy | 1 | NYGMN | 5 |
| | | | |
| Db | 2 | NYGMN | 6 |

```

RESULT 11
AAV17489
ID AAV17489 standard; peptide; 7 AA

```

| | |
|----|---------------------------|
| AC | AAV17489; |
| XX | |
| DT | 03-AUG-1999 (first entry) |

DE Mab 31.1 CDR sequence derived peptide COL311 H1.

KM Heavy chain variable region; 2C9NHC0L1, light chain variable region;
KM light chain consensus region; heavy chain consensus region; antibody
KM anti-idiotypic response; modified immunoglobulin; infectious disease;
KM cancer; vaccine.

OS Synthetic.

PN W09925379-A1.

PD 27-MAY-1999

PF 13-NOV-1998; 98WO-US024303.

PR 14-NOV-1997; 97US-0065716P.

PR 10-APR-1998; 98US-0081403P.

PA (EURO-) EUROCELLIQUE SA.

PI Burch RM;

DR WPI; 1999-337877/28.

PT Vaccines for generating an anti-idiotypic response to an antigen.

PS Example; Page 55; 107pp; English.

The present invention describes vaccines for generating an anti-idiotypic response to an antigen. Vaccine (A), comprises, apart from a carrier, a first immunoglobulin (I), comprising a variable region (V), or its fragment that includes V, which is identical to a second immunoglobulin (II), or its corresponding fragment, which can bind specifically to an antigen (Ag), except for one or more amino acid (aa) substitutions in V. These substitutions involve replacement of Cys residues involved in disulfide bridge formation by residues that do not contain a thiol group (A) are used to raise an anti-idiotypic response [preferably both cellular and humoral], particularly for treating a wide range of tumours (or precancerous conditions) and infectious diseases (viral, bacterial, fungal, parasitic), specifically syphilis, gonorrhea, acquired immune deficiency syndrome, malaria, Shigella, Salmonella, hepatitis A or C, Lyme disease, encephalitis, herpes, Gram-positive or -negative bacterial infections, or pneumococcal infections. Antibodies raised against the vaccine may be recovered and administered to a second subject. (I) may also be used for treating autoimmune diseases and allergy. Modifying (II) so that it can no longer form intrachain disulfide bridges reduces conformational constraints and results in significantly better anti-idiotypic responses. The present sequence represents a Mab 31.1 CDR sequence derived peptide from an example from the present invention

Sequence 7 AA:

| | | | | |
|-----------------------|---------|--------------------|-------|-----------|
| Query Match | 100.0%; | Score 30; | DB 2; | Length 7; |
| Best Local Similarity | 100.0%; | Pred. No. 1.8e+06; | | |

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|---|-------|---|
| QY | 1 | NYGMN | 5 |
| | | | |
| Db | 3 | NYGMN | 7 |

RESULT 12
AAY08698
ID AAY08698 standard; protein; 7 AA

AC AA008698

| | |
|----|---|
| DT | 10-AUG-1999 (first entry) |
| XX | |
| DE | Human colon carcinoma-associated protein antigen binding fragment 4 |

KW Immunoglobulin;

KW cellular rece

KW ulcerative c

human colon cancer-associated

XX

XX 3
ADAM
BAPTIST
CARR

XX

XX :
:
:
:
:

[illegible]

PR 10-APR-1998; 98US-0081403P.

PA (EURO-) EUROCELLIQUE S.A.

PA Burch RM,
 PT
 XX WPI; 1999-357555/30.
 XX
 XX
 XX
 PS
 PS Claim 6; Page 75; 123pp; English.
 CC This invention describes a novel modified immunoglobulin (mig), or its
 CC fragment, that binds immunospecifically to one member (M1) of a binding
 CC pair comprising a variable domain (V) having at least one CDR
 CC (complementarily determining region) that contains a portion of the
 CC second member (M2) of the pair. This portion is not present in the
 CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen
 CC a cellular receptor for an infectious agent (provided the binding site is
 CC not NAMP or NMDP) or a member of a receptor-ligand pair. mig (also
 CC related molecules containing the same V region), optionally coupled to a
 CC chemotherapeutic agent, are used in therapeutic and/or prophylactic
 CC compositions, or vaccines, against cancers, infectious or autoimmune
 CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or
 CC allergies. They can also be used as immunoassay reagents for diagnosing
 CC these conditions. mig can be used in human or veterinary medicine. mig
 CC have higher affinity or specificity than native antibodies. mig
 CC of CDR ensures binding specificity and avoids the unpredictable
 CC immunization and screening procedures currently used. It is now possible
 CC to generate antibodies against antigens that are inaccessible, by virtue
 CC of immune tolerance or cryptic expression. mig neutralize antigens
 CC directly or they induce an anti-idiotypic immune response. This sequence
 CC represents a fragment of modified immunoglobulin that immunospecifically
 CC binds to a binding pair in which the first member is the human colon
 CC carcinoma-associated protein antigen


```

XX
AC AAG80311;
XX
DT 18-FEB-2002 (first entry)
XX
DE Anti-human TNF-alpha CDR-H1 peptide.
XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO200179298-A1.
XX
PD 25-OCT-2001.
XX
PF 18-APR-2001; 2001WO-JP003308.
XX
PR 19-APR-2000; 2000JP-00117394.
XX
PA (SUNR ) SUNTORX LTD.
XX
PI Fukuda Y, Nagahira K, Nakanishi T;
XX
PI WPI; 2002-066345/09.
XX
DR
XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.
XX
PS Claim 1a; Page 25; 36pp; Japanese.
XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H1
XX
SQ Sequence 10 AA;

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Query Match 100.0%; Score 30; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.1;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NYGMN 5
   |||||
Db 6 NYGMN 10

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Search completed: April 4, 2005, 15:47:07
 Job time : 11.984 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 7.38019 Seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_31_35
Perfect score: 30
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues
Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 30 | 100.0 | 5 | 9 | US-09-965-099-8 |
| 2 | 30 | 100.0 | 5 | 10 | US-09-791-551-74 |
| 3 | 30 | 100.0 | 5 | 13 | US-10-051-852-8 |
| 4 | 30 | 100.0 | 5 | 14 | US-10-071-962-15 |
| 5 | 30 | 100.0 | 5 | 15 | US-10-430-176-8 |
| 6 | 30 | 100.0 | 5 | 15 | US-10-377-121-26 |
| 7 | 30 | 100.0 | 10 | 9 | US-09-056-1608-1 |
| 8 | 30 | 100.0 | 10 | 14 | US-10-234-671-1 |
| 9 | 30 | 100.0 | 10 | 16 | US-10-018-245A-1 |
| 10 | 30 | 100.0 | 10 | 16 | US-10-723-434-111 |
| 11 | 30 | 100.0 | 10 | 16 | US-10-723-434-112 |
| 12 | 30 | 100.0 | 10 | 16 | US-10-723-434-116 |
| 13 | 30 | 100.0 | 10 | 16 | US-10-723-434-122 |

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| 14 | 30 | 100.0 | 10 | 17 | US-10-687-035-60 | Sequence 60, App1 |
| 15 | 30 | 100.0 | 12 | 10 | US-09-954-385-147 | Sequence 147, App |
| 16 | 30 | 100.0 | 12 | 17 | US-10-912-512-147 | Sequence 147, App |
| 17 | 30 | 100.0 | 12 | 17 | US-10-235-043-147 | Sequence 147, App |
| 18 | 30 | 100.0 | 67 | 14 | US-10-243-130-19 | Sequence 17, App1 |
| 19 | 30 | 100.0 | 70 | 14 | US-10-243-130-17 | Sequence 17, App1 |
| 20 | 30 | 100.0 | 70 | 14 | US-10-243-130-18 | Sequence 17, App1 |
| 21 | 30 | 100.0 | 70 | 17 | US-10-901-650-17 | Sequence 18, App1 |
| 22 | 30 | 100.0 | 70 | 17 | US-10-901-650-18 | Sequence 18, App1 |
| 23 | 30 | 100.0 | 70 | 17 | US-10-901-650-19 | Sequence 19, App1 |
| 24 | 30 | 100.0 | 76 | 15 | US-10-424-559-268610 | Sequence 268610, |
| 25 | 30 | 100.0 | 92 | 13 | US-09-965-099-84 | Sequence 84, App1 |
| 26 | 30 | 100.0 | 92 | 13 | US-10-051-852-84 | Sequence 84, App1 |
| 27 | 30 | 100.0 | 92 | 15 | US-10-430-176-84 | Sequence 84, App1 |
| 28 | 30 | 100.0 | 112 | 9 | US-09-965-099-20 | Sequence 20, App1 |
| 29 | 30 | 100.0 | 112 | 13 | US-10-051-852-20 | Sequence 20, App1 |
| 30 | 30 | 100.0 | 112 | 15 | US-10-430-176-20 | Sequence 20, App1 |
| 31 | 30 | 100.0 | 116 | 9 | US-09-971-543-8 | Sequence 9, App1 |
| 32 | 30 | 100.0 | 116 | 9 | US-09-971-543-9 | Sequence 9, App1 |
| 33 | 30 | 100.0 | 116 | 9 | US-09-971-543-10 | Sequence 10, App1 |
| 34 | 30 | 100.0 | 116 | 14 | US-10-138-727A-2 | Sequence 2, App1 |
| 35 | 30 | 100.0 | 116 | 14 | US-10-138-727A-4 | Sequence 4, App1 |
| 36 | 30 | 100.0 | 116 | 14 | US-10-138-727A-6 | Sequence 6, App1 |
| 37 | 30 | 100.0 | 116 | 14 | US-10-138-727A-17 | Sequence 17, App1 |
| 38 | 30 | 100.0 | 116 | 14 | US-10-138-727A-18 | Sequence 18, App1 |
| 39 | 30 | 100.0 | 116 | 14 | US-10-138-727A-19 | Sequence 19, App1 |
| 40 | 30 | 100.0 | 116 | 14 | US-10-138-727A-20 | Sequence 20, App1 |
| 41 | 30 | 100.0 | 116 | 14 | US-10-138-727A-21 | Sequence 21, App1 |
| 42 | 30 | 100.0 | 116 | 14 | US-10-138-727A-22 | Sequence 22, App1 |
| 43 | 30 | 100.0 | 116 | 14 | US-10-138-727A-23 | Sequence 23, App1 |
| 44 | 30 | 100.0 | 116 | 14 | US-10-138-727A-24 | Sequence 24, App1 |
| 45 | 30 | 100.0 | 116 | 14 | US-10-138-727A-25 | Sequence 25, App1 |

ALIGNMENTS

RESULT 1
US-09-965-099-8
; Sequence 8, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Girola
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965, 099
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/346,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096

TELEFAX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-965-099-8

Query Match 100.0%; Score 30; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 2
US-09-791-551-74
Sequence 74, Application US/09791551
Publication No. US20030235584A1
GENERAL INFORMATION:
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
FILE REFERENCE: 037003/0277869
CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/185,390
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 5
TYPE: PRT
ORGANISM: Mus sp.
US-09-791-551-74

Query Match 100.0%; Score 30; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 3
US-10-051-852-8
Sequence 8, Application US/10051852
Publication No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
Patel, Atunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-051-852-8

Query Match 100.0%; Score 30; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 4
US-10-071-962-15
Sequence 15, Application US/10071962
Publication No. US20030170237A1
GENERAL INFORMATION:
APPLICANT: Bault N.
APPLICANT: Bault N.C. Sun
APPLICANT: Cedilly R.Y. Sun
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
TITLE OF INVENTION: Screening Method Therefor
FILE REFERENCE: 98-3
CURRENT APPLICATION NUMBER: US/10/071,962
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/303,155A
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,575
PRIOR FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 5

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/ TYPE: PRT
/ ORGANISM: mouse
US-10-071-962-15.

Query Match
Best Local Similarity 100.0%; Score 30; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 5
US-10-430-176-8
/ Sequence 8, Application US/10430176
/ Publication No. US20030235587A1
/ GENERAL INFORMATION:
/ APPLICANT: Feuerstein, Gloria Z.
/ TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
/ FILE REFERENCE: P50816-1
/ CURRENT APPLICATION NUMBER: US/10/430,176
/ CURRENT FILING DATE: 2003-05-05
/ PRIOR APPLICATION NUMBER: 09/817,960
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 09/359,202
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 60/095,714
/ PRIOR FILING DATE: 1998-08-07
/ PRIOR APPLICATION NUMBER: 10/051,852
/ PRIOR FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 09/344,050
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 08/783,853
/ PRIOR FILING DATE: 1997-01-06
/ PRIOR APPLICATION NUMBER: 60/010,018
/ PRIOR FILING DATE: 199-01-17
/ PRIOR APPLICATION NUMBER: 60/029,119
/ PRIOR FILING DATE: 1996-10-24
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-430-176-8

Query Match
Best Local Similarity 100.0%; Score 30; DB 15; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 6
US-10-377-121-26
/ Sequence 26, Application US/10377121
/ Publication No. US20040001825A1
/ GENERAL INFORMATION:
/ APPLICANT: GOVINDAM, SERENGULAM
/ APPLICANT: GU, ZHENGXING
/ APPLICANT: HANSEN, HANS
/ APPLICANT: GOLDENBERG, DAVID
/ TITLE OF INVENTION: RS7 ANTIBODIES
/ FILE REFERENCE: 018733/1163
/ CURRENT APPLICATION NUMBER: US/10/377,121
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: 60/360,299
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 36
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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Mus sp.
US-10-377-121-26

Query Match
Best Local Similarity 100.0%; Score 30; DB 15; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5
Db 1 NYGMN 5

RESULT 7
US-09-056-160B-1
/ Sequence 1, Application US/09056160B
/ Patent No. US20020032315A1
/ GENERAL INFORMATION:
/ APPLICANT: Baca, Manuel
/ APPLICANT: Wells, James A.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Chen, Yvonne M.
/ TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
/ NUMBER OF SEQUENCES: 131
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/056,160B
/ FILING DATE: 06-Apr-1998
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/054,856
/ FILING DATE: 06-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hasek, Janet E.
/ REGISTRATION NUMBER: 28,616
/ REFERENCE/DOCKET NUMBER: P1093R2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1896
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-09-056-160B-1

Query Match
Best Local Similarity 100.0%; Score 30; DB 9; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5
Db 6 NYGMN 10

RESULT 8
US-10-234-671-1
/ Sequence 1, Application US/10234671
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/ Publication No. US20030190317A1
/ GENERAL INFORMATION:
/ APPLICANT: Baca, Manuel
/               Wells, James A.
/               Presta, Leonard G.
/               Lowman, Henry B.
/               Chen, Yvonne M.
/ TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
/ NUMBER OF SEQUENCES: 131
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/234,671
/ FILING DATE: 03-Sep-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/056160
/ FILING DATE: 06-APR-1998
/ APPLICATION NUMBER: 60/126446
/ FILING DATE: 07-APR-1997
/ APPLICATION NUMBER: 60/054856
/ FILING DATE: 06-AUG-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cui, Steven X.
/ REGISTRATION NUMBER: 44,637
/ REFERENCE/DOCKET NUMBER: P1093R2C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-8674
/ TELEFAX: 650/952-9881
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
/ US-10-234-671-1
/
Query Match      100.0%; Score 30; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NYGMN 5
Db      6 NYGMN 10

RESULT 9
US-10-018-245A-1
/ Sequence 1, Application US/10018245A
/ Publication No. US20040115196A1
/ GENERAL INFORMATION:
/ APPLICANT: FUKUDA, Yoshiaki
/ APPLICANT: NAKAHARA, Kazuhiko
/ APPLICANT: NAKANISHI, Toshihiro
/ TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
/ TITLE OF INVENTION: determining regions and genes encoding the same
/ FILE REFERENCE: 46224
/ CURRENT APPLICATION NUMBER: US/10/018,245A
/ CURRENT FILING DATE: 2002-07-12
/ PRIOR APPLICATION NUMBER: JP 117394/2000
/ PRIOR FILING DATE: 2000-04-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatencIn Ver. 2.1
```

```
/ SEQ ID NO: 1
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: mouse
/ FEATURE:
/ OTHER INFORMATION: CDR-H1 of anti-human TNF-alpha antibody
/ US-10-018-245A-1
/
Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NYGMN 5
Db      6 NYGMN 10

RESULT 10
US-10-723-434-111
/ Sequence 111, Application US/10723434
/ Publication No. US2004013357A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Wang, Kevin C.
/ APPLICANT: Hsieh, Mark
/ APPLICANT: Li, Yan
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
/ FILE REFERENCE: 26050-709.501
/ CURRENT APPLICATION NUMBER: US/10/723,434
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 60/284,407
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: US 10/125,687
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: US 10/153,176
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US 10/443,134
/ PRIOR FILING DATE: 2003-05-20
/ NUMBER OF SEQ ID NOS: 156
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 111
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VH/CDR1
/ US-10-723-434-111
/
Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NYGMN 5
Db      6 NYGMN 10

RESULT 11
US-10-723-434-112
/ Sequence 112, Application US/10723434
/ Publication No. US2004013357A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhong, Pingyu
/ APPLICANT: Luo, Peizhi
/ APPLICANT: Wang, Kevin C.
/ APPLICANT: Hsieh, Mark
/ APPLICANT: Li, Yan
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
/ FILE REFERENCE: 26050-709.501
/ CURRENT APPLICATION NUMBER: US/10/723,434
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 60/284,407
```


;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; PRIOR FILING DATE: 2003-05-20
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 112
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH/CDR1
US-10-723-434-112

Query Match 100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 6 NYGMN 10

RESULT 12
US-10-723-434-116
;; Sequence 116, Application US/10723434
;; Publication No. US2004013357A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhong, Pingyu
;; APPLICANT: Luo, Peizhi
;; APPLICANT: Wang, Kevin C.
;; APPLICANT: Hsieh, Mark
;; APPLICANT: Li, Yan
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
;; FILE REFERENCE: 26050-709, 501
;; CURRENT APPLICATION NUMBER: US/10/723,434
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 116
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH/CDR1
US-10-723-434-116

Query Match 100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 6 NYGMN 10

RESULT 13
US-10-723-434-122
;; Sequence 122, Application US/10723434
;; Publication No. US2004013357A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhong, Pingyu

;; APPLICANT: Luo, Peizhi
;; APPLICANT: Wang, Kevin C.
;; APPLICANT: Hsieh, Mark
;; APPLICANT: Li, Yan
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
;; FILE REFERENCE: 26050-709, 501
;; CURRENT APPLICATION NUMBER: US/10/723,434
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 122
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH/CDR1
US-10-723-434-122

Query Match 100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 6 NYGMN 10

RESULT 14
US-10-687-035-60
;; Sequence 60, Application US/10687035
;; Publication No. US20050064518A1
;; GENERAL INFORMATION:
;; APPLICANT: Albane, Earl F.
;; APPLICANT: Solcic, Daniel A.
;; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
;; FILE REFERENCE: 6750-214-999
;; CURRENT APPLICATION NUMBER: US/10/687,035
;; PRIOR FILING DATE: 2003-10-15
;; PRIOR APPLICATION NUMBER: 60/485,986
;; PRIOR FILING DATE: 2003-07-10
;; PRIOR APPLICATION NUMBER: 60/418,828
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 60
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 725.1 VH1 CDR
US-10-687-035-60

Query Match 100.0%; Score 30; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 6 NYGMN 10

RESULT 15
US-09-954-385-147
;; Sequence 147, Application US/09954385

; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselte G. J.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-147

Query Match 100.0%; Score 30; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||
Db 6 NYGMN 10

Search completed: April 4, 2005, 16:42:43
Job time : 8.38019 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 1.80511 seconds

(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_31_35

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 30 | 100.0 | 93 | 2 C24672 | Ig heavy chain V r |
| 2 | 30 | 100.0 | 99 | 2 S26326 | Ig heavy chain V r |
| 3 | 30 | 100.0 | 101 | 2 D24672 | Ig heavy chain V r |
| 4 | 30 | 100.0 | 105 | 2 S24764 | Ig heavy chain V r |
| 5 | 30 | 100.0 | 105 | 2 S24765 | Ig heavy chain V r |
| 6 | 30 | 100.0 | 109 | 2 S26325 | Ig heavy chain V r |
| 7 | 30 | 100.0 | 115 | 2 S19968 | Ig heavy chain V r |
| 8 | 30 | 100.0 | 115 | 2 S19965 | Ig heavy chain V r |
| 9 | 30 | 100.0 | 116 | 2 S63305 | Ig heavy chain V r |
| 10 | 30 | 100.0 | 118 | 2 S19967 | Ig heavy chain V r |
| 11 | 30 | 100.0 | 119 | 2 A53285 | Ig heavy chain V a |
| 12 | 30 | 100.0 | 120 | 2 B42848 | Ig mb heavy chain |
| 13 | 30 | 100.0 | 120 | 2 S12953 | Ig heavy chain V r |
| 14 | 30 | 100.0 | 124 | 2 PH1404 | Ig heavy chain V r |
| 15 | 30 | 100.0 | 146 | 4 S33905 | Ig heavy chain pre |
| 16 | 30 | 100.0 | 398 | 2 B90406 | geranylgeranyl hyd |
| 17 | 30 | 100.0 | 725 | 2 S01042 | deribactin recepto |
| 18 | 30 | 100.0 | 726 | 2 AB0122 | probable ferric si |
| 19 | 30 | 100.0 | 732 | 2 T44483 | receptor-like prot |
| 20 | 27 | 90.0 | 96 | 2 B90793 | hypothetical prote |
| 21 | 27 | 90.0 | 96 | 2 G85653 | hypothetical prote |
| 22 | 27 | 90.0 | 151 | 2 E70615 | hypothetical prote |
| 23 | 27 | 90.0 | 153 | 2 G75616 | hypothetical prote |
| 24 | 27 | 90.0 | 174 | 2 P85028 | modulation protein |
| 25 | 27 | 90.0 | 191 | 2 A97074 | hypothetical prote |
| 26 | 27 | 90.0 | 212 | 2 D84442 | probable glutathio |
| 27 | 27 | 90.0 | 281 | 2 S34496 | hypothetical prote |
| 28 | 27 | 90.0 | 321 | 2 D97836 | tetraacyldisacchar |
| 29 | 27 | 90.0 | 326 | 1 VGXR37 | glycoprotein VP7 p |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 27 | 90.0 | 326 | 1 VGXR7H | glycoprotein VP7 p |
| 31 | 27 | 90.0 | 326 | 1 VGXRMD | glycoprotein VP7 p |
| 32 | 27 | 90.0 | 326 | 1 VGXRWA | glycoprotein VP7 p |
| 33 | 27 | 90.0 | 329 | 2 T13016 | hypothetical prote |
| 34 | 27 | 90.0 | 338 | 2 T28779 | hypothetical prote |
| 35 | 27 | 90.0 | 340 | 2 T28080 | hypothetical prote |
| 36 | 27 | 90.0 | 344 | 2 H45252 | p1ly constant regi |
| 37 | 27 | 90.0 | 373 | 2 A63143 | galactosyl-transfe |
| 38 | 27 | 90.0 | 381 | 2 T40341 | hypothetical prote |
| 39 | 27 | 90.0 | 388 | 2 A82903 | conserved hypothet |
| 40 | 27 | 90.0 | 391 | 2 E83840 | hypothetical prote |
| 41 | 27 | 90.0 | 406 | 2 JCA600 | isocitrate dehydro |
| 42 | 27 | 90.0 | 454 | 2 A97147 | siderophore/Surfac |
| 43 | 27 | 90.0 | 470 | 1 S14628 | phosphogluconate d |
| 44 | 27 | 90.0 | 560 | 2 S09995 | nuclear factor I-B |
| 45 | 27 | 90.0 | 561 | 2 A31256 | transcription fact |

ALIGNMENTS

RESULT 1

C24672 Ig heavy chain V region (YMU-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: C24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: C24672

A/Molecule type: DNA

A/Residues: 1-93 <MIN>

A/Cross-references: GB:X03300; NID:952375; PIDN:CAA27039.1; PID:9773221

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 12 NYGMN 16

RESULT 2

S26326 Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998

C/Accession: S26326

R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ei

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26326

A/Molecule type: mRNA

A/Residues: 1-99 <STA>

A/Cross-references: EMBL:X59174

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 99;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 11 NYGMN 15

RESULT 3

D24672

Ig heavy chain V region (VGAM3-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: D24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 <MIN>

A/Cross-references: GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

C/Keywords: heterotrimer; immunoglobulin

A/Accession: S24765
A/Molecule type: DNA
A/Residues: 1-105 <KLA>
A/Cross-references: EMBL:Z15001
A/Accession: S24773
A/Molecule type: DNA
A/Residues: 1-105 <KLM>
A/Cross-references: EMBL:Z15013
R/Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A/Reference number: S24776
A/Accession: S24778
A/Molecule type: DNA
A/Residues: 1-105 <THO>
A/Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620
A/Note: this sequence was determined from the differentiated gene
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
11111
Db 43 NYGMN 47

RESULT 6

S26325

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S26325

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Molecule type: preliminary

A/Status: preliminary

A/Residues: 1-109 <STA>

A/Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:G52080; PID:G1334043

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/5-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
11111
Db 21 NYGMN 25

RESULT 7

S19968

Ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: S19968

R/Weissenborn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: S19963

A/Accession: S19968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 <WEI>

A/Cross-references: UNIPROT:Q921A6; EMBL:X55089

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin
P:10-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
DB 26 NYGMN 30

RESULT 8
S19965
Ig heavy chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S19965
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19965
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <WEI>
A:Cross-references: UNIPROT:Q921A6; EMBL:X65088
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:8-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
DB 24 NYGMN 28

RESULT 9
S69305
Hypotheetical protein YLR280c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypotheetical protein L8003.10-b
C:Species: Saccharomyces cerevisiae
C:Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: S69305
R:Pauley, A.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 8003.
A:Reference number: S50366
A:Accession: S69305
A:Molecule type: DNA
A:Residues: 1-116 <PAU>
A:Cross-references: UNIPROT:Q13541; EMBL:U17243; NID:G596030; PTDN:AA67350.1; PID:G2340
C:Genetics:
A:Gene: MIPS:YLR280c
A:Cross-references: SGD:S0004270
A:Map position: 12R
C:Superfamily: Saccharomyces hypotheetical protein YLR280c

Query Match 100.0%; Score 30; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
DB 19 NYGMN 23

RESULT 10
S19967
Ig heavy chain V region (M-T406) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S19967
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19967
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <WEI>

A:Cross-references: UNIPROT:Q921A6; EMBL:X65090
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
DB 28 NYGMN 32

RESULT 11
A53285
Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53285
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct
and their pH-reactivity profiles.
A:Reference number: A53285; MUID:92017897; PMID:1922102
A:Accession: A53285
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-119 <SAW>
A:Cross-references: GB:D12736; NID:G220595; PTDN:BA02228.1; PID:G220596
A:Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:P:63299)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
|||||
DB 31 NYGMN 35

RESULT 12
B42848
L6 mAb heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B42848; S33903
R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,
J. Biol. Chem. 267, 15552-15558, 1992
A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character
A:Reference number: A42848; MUID:92348410; PMID:1639794
A:Accession: B42848
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <FEI>
A:Cross-references: GB:M90690; NID:G195065; PTDN:AAA38146.1; PID:G195066
A:Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P:109961)
A:Accession: S33903
A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <FE2>

A:Cross-references: EMBL:M90691

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

100.0%; Score 30; DB 2; Length 120;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 31 NYGMN 35

RESULT 13

S12953

Ig heavy chain V region (Y13-259) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C:Accession: S12953

R:Merge, T.M.; Biocca, S.; Cattaneo, A.

FEBS Lett. 274, 193-198, 1990

A>Title: Intracellular immunization. Cloning and intracellular expression of a monoclonal

A:Reference number: S12953; MUID:91071431; PMID:2123805

A:Accession: S12953

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-120 <NER>

A:Cross-references: GB:X55179; NID:g56471; PIDN:CAA38964.1; PID:g56472

A>Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

100.0%; Score 30; DB 2; Length 120;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 31 NYGMN 35

RESULT 14

PH1404

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000

C:Accession: PH1404; PH1406

R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Taniguchi, M.; Taniguchi, M.

J. Exp. Med. 176, 1209-1214, 1992

A>Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in

la virus.

A:Reference number: PH1403; MUID:93018837; PMID:1402663

A:Accession: PH1404

A:Molecule type: DNA

A:Residues: 1-124 <SH1>

A:Accession: PH1406

A:Molecule type: DNA

A:Residues: 115-121 <SH2>

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 31 NYGMN 35

Db 51 NYGMN 55

RESULT 15
S33905
Ig heavy chain precursor V region - synthetic

C:Species: synthetic

C>Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000

C:Accession: S33905

R:Lin, A.Y.; Robinson, R.R.; Hellstrom, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstrom,

Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987

A>Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.

A:Reference number: S33905; MUID:87204152; PMID:3106970

A:Accession: S33905

A:Molecule type: mRNA

A:Residues: 1-146 <LIU>

A:Cross-references: EMBL:M16072; NID:g195270; PIDN:AAA38229.1; PID:g195271

Query Match 100.0%; Score 30; DB 4; Length 146;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 50 NYGMN 54

Search completed: April 4, 2005, 15:58:00
Job time : 2.80511 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 8.45048 Seconds

(Without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_31_35
Perfect score: 30
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 30 | 100.0 | 116 | 2 | 013541 |
| 2 | 30 | 100.0 | 175 | 1 | HIS5_BUCDN |
| 3 | 30 | 100.0 | 226 | 6 | Q73D74 |
| 4 | 30 | 100.0 | 244 | 2 | Q65L51 |
| 5 | 30 | 100.0 | 261 | 2 | Q6WDX4 |
| 6 | 30 | 100.0 | 299 | 2 | Q924G6 |
| 7 | 30 | 100.0 | 300 | 2 | Q6WDM3 |
| 8 | 30 | 100.0 | 301 | 2 | Q6WDM2 |
| 9 | 30 | 100.0 | 302 | 2 | Q924G5 |
| 10 | 30 | 100.0 | 305 | 2 | Q895E8 |
| 11 | 30 | 100.0 | 316 | 2 | Q9CLC4 |
| 12 | 30 | 100.0 | 323 | 2 | Q8XSL6 |
| 13 | 30 | 100.0 | 326 | 2 | Q39726 |
| 14 | 30 | 100.0 | 326 | 2 | Q85033 |
| 15 | 30 | 100.0 | 326 | 2 | Q95379 |
| 16 | 30 | 100.0 | 332 | 2 | Q814Y5 |
| 17 | 30 | 100.0 | 341 | 2 | Q9N2S8 |
| 18 | 30 | 100.0 | 342 | 2 | Q8XNS7 |
| 19 | 30 | 100.0 | 387 | 2 | Q6SHS8 |
| 20 | 30 | 100.0 | 398 | 2 | Q97W83 |
| 21 | 30 | 100.0 | 422 | 2 | Q7URZ8 |
| 22 | 30 | 100.0 | 423 | 2 | Q975B4 |
| 23 | 30 | 100.0 | 479 | 2 | Q7SBB0 |
| 24 | 30 | 100.0 | 725 | 2 | Q6J3R6 |
| 25 | 30 | 100.0 | 726 | 2 | Q66619 |
| 26 | 30 | 100.0 | 726 | 2 | Q8ZHB0 |
| 27 | 30 | 100.0 | 729 | 2 | Q8KR53 |
| 28 | 30 | 100.0 | 731 | 2 | Q7UB05 |
| 29 | 30 | 100.0 | 731 | 2 | Q6D8U6 |
| 30 | 30 | 100.0 | 732 | 1 | IURA_ECOLI |
| 31 | 30 | 100.0 | 732 | 2 | Q93PE2 |

| | | | | | | |
|----|----|-------|------|---|--------|--------------------|
| 32 | 30 | 100.0 | 732 | 2 | Q6Q7N8 | Q6Q7N8 escherichia |
| 33 | 30 | 100.0 | 732 | 2 | Q9XCH0 | Q9XCH0 shigella fl |
| 34 | 30 | 100.0 | 733 | 2 | Q6KDX4 | Q6KDX4 escherichia |
| 35 | 30 | 100.0 | 733 | 2 | Q6U607 | Q6U607 klebsiella |
| 36 | 30 | 100.0 | 759 | 2 | Q83PM3 | Q83PM3 shigella fl |
| 37 | 30 | 100.0 | 759 | 2 | Q8FDW0 | Q8FDW0 escherichia |
| 38 | 30 | 100.0 | 828 | 2 | Q8EX93 | Q8EX93 drosophila |
| 39 | 30 | 100.0 | 828 | 2 | Q9VBY0 | Q9VBY0 drosophila |
| 40 | 30 | 100.0 | 1119 | 2 | Q815N6 | Q815N6 plasmodium |
| 41 | 30 | 100.0 | 1133 | 2 | Q6CWR8 | Q6CWR8 kluyveromyc |
| 42 | 30 | 100.0 | 1480 | 2 | Q7RN37 | Q7RN37 plasmodium |
| 43 | 30 | 100.0 | 1959 | 2 | Q8V3G5 | Q8V3G5 swinepox vi |
| 44 | 27 | 90.0 | 36 | 2 | Q809B8 | Q809B8 human rotav |
| 45 | 27 | 90.0 | 36 | 2 | Q809C3 | Q809C3 human rotav |

ALIGNMENTS

RESULT 1

013541 PRELIMINARY; PRT; 116 AA.
AC 013541;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Y1280CP.
GN Name=Y1280CP;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Emtian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Weitzel D., Hilbert H., Hilger F., Kline K., Kotter P.,
RA Louis B.J., Messenguy F., Mewes H.W., Mloaga T., Mostl D.,
RA Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechemann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwaiger C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhaesselt P.,
RA Viendeeels F., Voet M., Voickaert G., Voss H., Wandut R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hant J., Hohnsbeil J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RN Nature 387:0-0(0).
RL
RN [2]
RP SEQUENCE FROM N.A.
RA Pauley A.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, U17243; AAB67350.1; -.
DR PIR, S69305; S69305.
SQ SEQUENCE 116 AA; 12951 MW; E31414157730E032 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 19 NYGMN 23

```

RESULT 2
HIS5_BUCDN
ID HIS5_BUCDN STANDARD; PRT; 175 AA.
AC Q84156;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (tmGP synthase subunit hisH) (IGP subunit hisH) (Fragment).
GN Name=hisH;
OS Buchnera aphidicola (subsp. Dittaphis noxia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OC NCBI_TaxID=118101;
RN (1)
RP SEQUENCE FROM N.A.
RA Moran N.A., Mira A.;
RT "Levels of selection on genes of mutualistic endosymbionts.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IGP synthase catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate. The hisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hisH for the synthesis of IGP and AICAR (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyxylulose-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF465524; AA033042.1; -.
CC DR HAMAP; MF_00278; -.1.
CC DR InterPro; IPR000991; GATase_1.
CC DR InterPro; IPR010139; IMP_synth_hisH.
CC DR Pfam; PF00117; GATase; 1.
CC DR TIGRPFAM; TIGR01855; IMP_synth_hisH; 1.
CC DR PROSITE; PS00442; GATASE_TYPE_I; 1.
CC DR Glutamine amidotransferase; Histidine biosynthesis; Transferase.
FT ACT_SITE 78 78 By similarity.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19540 MW; E50851BA299D89C3 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. NO. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 159 NYGMN 163

RESULT 3
Q73DT4 PRELIMINARY; PRT; 226 AA.
ID Q73DT4;
AC Q73DT4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCR0627;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

```

```

OX NCBI_TaxID=222523;
RN (1)
RP SEQUENCE FROM N.A.
RA PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raske D.A., Ravel J., Oekstad O.A., Helgeson E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolseoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017266; AAS39561.1; -.
DR TIGR; BCE0627; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 226 AA; 25834 MW; 9CCB16555AD97185 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 218 NYGMN 222

RESULT 4
Q65L51 PRELIMINARY; PRT; 244 AA.
ID Q65L51;
AC Q65L51;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein (Peptidoglycan-binding LysoM, Peptidoglycan-binding LysoM).
GN ORFNames=BL01953, BL401309;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Velth B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.U.,
RA Tang W., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU40223.1; -.
DR EMBL; CP000002; AAU22864.1; -.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 25925 MW; 1561DF7670470E2 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 42 NYGMN 46

RESULT 5

```



```
OGWDM4
ID OGWDM4 PRELIMINARY; PRT; 261 AA.
AC OGWDM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Acomya ignita (fifty spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Acomys.
OX NCBI_TaxID=60745;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY294923; AAQ62681.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 261
FT NON_TER 261
SQ SEQUENCE 261 AA; 28136 MW; F3641198C9807A3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 261;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 185 NYGMN 189

RESULT 6
Q924G6 PRELIMINARY; PRT; 299 AA.
ID O924G6;
AC Q924G6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Meriones shawi (Shaw's jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=37435;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21219190; PubMed=11319262;
RA Adkins R.M., Galke E.L., Rowe D., Honeycutt R.L.;
RT "Molecular phylogeny and divergence time estimates for major rodent
RT groups: evidence from multiple genes.";
RL Mol. Biol. Evol. 18:777-791(2001).
DR EMBL; AF332021; AAK71897.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 299
FT NON_TER 299
SQ SEQUENCE 299 AA; 32452 MW; 5E624460D1D7243E CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 299;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 198 NYGMN 202

RESULT 7
Q6WDM3 PRELIMINARY; PRT; 300 AA.
ID Q6WDM3;
AC Q6WDM3;
```

```
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Beania hindel (long-tailed pouched rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Beania.
OX NCBI_TaxID=70596;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY294904; AAQ62682.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 300
FT NON_TER 300
SQ SEQUENCE 300 AA; 32730 MW; 5211AC3F179BA984 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 300;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 199 NYGMN 203

RESULT 8
Q6WDM2 PRELIMINARY; PRT; 301 AA.
ID Q6WDM2;
AC Q6WDM2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Cricetomys gambianus (Gambia rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Cricetomys.
OX NCBI_TaxID=10085;
RN [1]
RP SEQUENCE FROM N.A.
RA Steppan S.J., Adkins R.M., Anderson J.;
RL Submitted (May-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY294905; AAQ62663.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 301
FT NON_TER 301
SQ SEQUENCE 301 AA; 32706 MW; F599E104ECAF857D CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 301;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 200 NYGMN 204

RESULT 9
Q924G5 PRELIMINARY; PRT; 302 AA.
ID Q924G5;
AC Q924G5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
```

OS Gerbillurus valliianus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Gerbillurus.
OX NCBI_TaxID=49440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21219190; PubMed=11319262;
RA Akins R.M., Gelke E.L., Rowe D., Honeycutt R.L.;
RT "Molecular phylogeny and divergence time estimates for major rodent
RT groups: evidence from multiple genes";
RL Mol. Biol. Evol. 18:777-791(2001).
DR EMBL; AF332022; AAK71898.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER 1
FT NON_TER 302
SQ SEQUENCE 302 AA; 32687 MW; C08D7478B24CEAC3 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 201 NYGMN 205
|||||
RESULT 10
Q895E8 PRELIMINARY; PRT; 305 AA.
ID Q895E8
AC Q895E8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Hypoetical protein CTC01328.
GN OrderedlocusNames=CTC01328;
OS Clostridium tetrani;
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / B88;
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA Brueggemann H., Baumer S., Fricke W.F., Wiese A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetrani, the causative agent of
RT tetanus disease";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AB015940; AAO35892.1; -.
KW Complete proteome.
SQ SEQUENCE 305 AA; 34802 MW; 6AEC3E38786B98D8 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 24 NYGMN 28
|||||
RESULT 11
Q9CLC4 PRELIMINARY; PRT; 316 AA.
ID Q9CLC4
AC Q9CLC4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CorA.
GN Name=CorA; OrderedlocusNames=PM1315;

OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AB061700; AAK03399.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015087; F:cobalt ion transporter activity; IEA.
DR GO; GO:0015095; F:magnesium ion transporter activity; IEA.
DR GO; GO:0006824; P:cobalt ion transport; IEA.
DR GO; GO:0015693; P:magnesium ion transport; IEA.
DR InterPro; IPR004488; CorA transp.
DR InterPro; IPR002523; Mg2+_transpCorA.
DR Pfam; PF01544; CorA; 1.
DR TIGRPFAM; TIGR00383; CorA; 1.
KW Complete proteome.
SQ SEQUENCE 316 AA; 36422 MW; AD3EFA4BC0ACC99 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 275 NYGMN 279
|||||
RESULT 12
Q8XS16 PRELIMINARY; PRT; 323 AA.
ID Q8XS16
AC Q8XS16;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PROBABLE MAGNESIUM AND COBALT TRANSMEMBRANE PROTEIN.
GN Name=RS01784; OrderedlocusNames=RS0665;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMT1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Arlat M., Billault A., Broctier P., Camus J.C., Cattellico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunne S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
DR EMBL; AL646080; CAD17816.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0046873; F:metal ion transporter activity; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
DR Pfam; PF01544; CorA; 1.
KW Complete proteome.
SQ SEQUENCE 323 AA; 36251 MW; DE264559E199D61 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 1 NYGMN 5
|||||

Db 282 NYGMN 286

RESULT 13

ID 039726 PRELIMINARY; PRT; 326 AA.
AC 039726;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE VP7.
OS Human rotavirus G3.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A.
OX NCBI_TaxID=73036;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97412814; PubMed=9267457;
RA Wen L., Nakayama M., Yamashita Y., Nishio O., Fang Z.-Y., Nakagomi O.,
RA Araki K., Nishimura S., Hasegawa A., Muller W.E., Ushijima H.;
RL Arch. Virol. 142:1481-1489 (1997).
RT "Genetic variation in the VP7 gene of human rotavirus serotype 3 (G3
type) isolated in China and Japan."
DR EMBL; D86274; BAA23294.1; -
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37318 MW; ED2375A2CBA14234 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5
DB 52 NYGMN 56

RESULT 14

ID 085033 PRELIMINARY; PRT; 326 AA.
AC 085033;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Outer capsid protein VP7.
OS Porcine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10913;
RN [1]
RP SEQUENCE FROM N.A.
RA Claret M., Luder J.E., Liprandi F.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L35057; AAA47091.1; -
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37078 MW; 36A21B861A8F8B3E CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5
DB 52 NYGMN 56

RESULT 15

ID 09E3T9 PRELIMINARY; PRT; 326 AA.
AC 09E3T9;

DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Outer capsid protein VP7.
OS Human rotavirus A.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97/S48;
RA Xu S., Wang J., Hung T.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260957; AAG15360.1; -
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37285 MW; 19479E95DAD21507 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5
DB 52 NYGMN 56Search completed: April 4, 2005, 15:56:03
Job time : 11.4505 secs

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CC Present sequence represents a VH domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 97; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||
DB 50 WINTYTGSTYADDFKE 66

RESULT 2

AAW02280
ID AAW02280 standard; protein; 243 AA.

AC AAW02280;

DT 25-MAR-2003 (revised)
DT 29-OCT-1996 (first entry)

DE 520C9 anti-c-erbB-2 two single chain Fv construct.

KM 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;
KM construct; polypeptide linker; C-terminal amino acid sequence;
KM in vivo imaging; drug targeting experiment; homodimer; increased;
KM binding avidity; tissue retention time.

OS Homo sapiens.

Key Location/Qualifiers
FT Peptide 118..133
/label= linker

US5534254-A.

09-JUL-1996.

07-OCT-1993; 93US-00133804.

06-FEB-1992; 92US-00831967.

PA (CHIR) CHIRON CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1996-333194/73.

DR N-PSDB; AAT36880.

PT Compens. contg. antigen-targeting antibody fragment constructs -
PT comprising dimer of single-chain Fv fragments.

PS Example 1; Col 33-36; 30pp; English.

CC Variable heavy (VH) and variable light (VL) genes were cloned from a
CC 520C9 hybridoma cDNA library, using probes directed toward the antibody
CC constant and joining regions. A two single chain Fv (sfv) gene was
CC constructed by connecting the VH and VL genes with a Ser rich polypeptide
CC linker. The resulting 520C9 two sfv gene, which encodes the present
CC sequence, was inserted into an expression vector, transformed into E.
CC coli, and protein expression induced by the addn. of IPTG to the culture
CC medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv
CC protein prod. is a homodimer, in which both fragments target the same
CC antigen, therefore giving greater binding avidity and longer tissue
CC retention times, compared to individual sfv protein prod. fragments.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 97; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||
DB 50 WINTYTGSTYADDFKE 66

RESULT 3

AAW53170
ID AAW53170 standard; protein; 243 AA.

AC AAW53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KM Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;
KM tumour; diagnosis; sg.

OS Synthetic.

OS Mus sp.

PN US5753204-A.

XX 19-MAY-1998.

05-JUN-1995; 95US-00461838.

06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR) CHIRON CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1998-311318/27.

DR N-PSDB; AAV21798.

PT Imaging of antigens in vivo - using dimers of single-chain antibody Fv
PT fragments.

PS Example 1; Col 33-36; 30pp; English.

CC This represents the protein sequence of a 520C9 sfv' (single chain Fv)
CC construct. This was constructed by connecting the VH and VL genes with a
CC DNA sequence encoding a serine rich linker. 520C9 is a monoclonal
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can
CC be used in the methods of invention of imaging a preselected antigen
CC expressed in a mammal. The methods are used in magnetic resonance imaging
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
CC constructs have enhanced properties as in vivo targeting agents in
CC comparison with intact monoclonal antibodies or their Fab fragments. The
CC dimeric constructs permit the in vivo targeting of an epitope on an
CC antigen with greater apparent avidity, including greater tumour
CC specificity, tumour localisation and tumour retention properties than
CC that of the Fab fragment having the same CDRs as the construct
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 97; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||
DB 50 WINTYTGSTYADDFKE 66

RESULT 4

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AAW80424
ID AAW80424 standard; protein; 243 AA.
XX
AC AAW80424;
XX
DT 28-JAN-1999 (first entry)
XX
DE 520C9 sFV sequence.
XX
KW 520C9 sFV; antigen; tumour cell; antibody 520C9; targeted delivery;
XX antigen-expressing cell.
XX
OS Synthetic.
XX
PN US5837846-A.
XX
PD 17-NOV-1998.
XX
PF 05-JUN-1995; 95US-00461386.
XX
PR 06-FEB-1992; 92US-00831967.
XX PR 07-OCT-1993; 93US-00133804.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CHIR ) CHIRON CORP.
PI Oppermann H, Houston LL, Huston JS, Ring DB;
XX
XX WPI; 1999-023541/02.
DR N-PSDB; AAV63399.
XX
XX Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
XX especially to tumours.
XX
XX Example 1; Col 35-36; 29pp; English.
XX
XX The present sequence represents an antibody 520C9 sFV. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs
CC or 99m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumours (especially of ovary or breast)
XX
XX Sequence 243 AA;
SQ
Query Match 100.0%; Score 97; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WINTYTGOSTVADDFKE 17
DB 50 WINTYTGOSTVADDFKE 66
RESULT 5
ABW00716
ID ABW00716 standard; protein; 243 AA.
XX
AC ABW00716;
XX
DT 15-JAN-2004 (first entry)
XX
DE 520C9 sFV protein.
XX
KW Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
XX sFV.
XX Unidentified.
XX
XX US2002168375-A1.
PN

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XX
PD 14-NOV-2002.
XX
XX 21-JUN-2001; 2001US-00887853.
XX
XX 06-FEB-1992; 92US-00831967.
XX PR 07-OCT-1993; 93US-00133804.
XX PR 05-JUN-1995; 95US-00462641.
XX PR 26-APR-2000; 2000US-00558741.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX WPI; 2003-765156/72.
DR N-PSDB; AAD61485.
XX
XX Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
XX Example 1; Page 19-20; 30pp; English.
XX
XX The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibit cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 sFV protein. This sequence is used in the exemplification of the
XX invention
XX
XX Sequence 243 AA;
SQ
Query Match 100.0%; Score 97; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WINTYTGOSTVADDFKE 17
DB 50 WINTYTGOSTVADDFKE 66
RESULT 6
AAR39569
ID AAR39569 standard; protein; 246 AA.
XX
XX AAR39569;
XX
XX 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
XX Sequence of 520C9 sFV protein.
XX
XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW biosynthetic single polypeptide chain binding site; ss.
XX
XX Synthetic.
XX
XX WO9316185-A2.
XX
XX 19-AUG-1993.
XX
XX 05-FEB-1993; 93WO-US001055.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU ) CETUS ONCOLOGY CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX

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| Query Match | Best Local Similarity | Score 97; | DB 2; | Length 246; |
|-------------|--|---|---------------|-------------|
| Matches 17; | Conservative | 0; | Mismatches 0; | Indels 0; |
| Gaps 0; | | | | |
| Qy | 1 WINTYTGOSTYADDFKE 17 | | | |
| | | | | |
| Db | 50 WINTYTGOSTYADDFKE 66 | | | |
| RESULT 7 | | | | |
| AAU04944 | AAU04944 | standard; | protein; | 267 AA. |
| XX | AAU04944; | | | |
| XX | | | | |
| DT | 06-AUG-2003 (revised) | | | |
| DT | 24-OCT-2001 (first entry) | | | |
| XX | | | | |
| DE | Humanised anti-p185 single chain antibody, 520C9H. | | | |
| XX | | | | |
| XX | Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate; | | | |
| KW | cancer; tumour; adenocarcinoma. | | | |
| XX | | | | |
| OS | Homo sapiens. | | | |
| OS | Mus sp. | | | |
| OS | Synthetic. | | | |
| OS | Chimeric. | | | |
| XX | | | | |
| FT | Key | Location/Qualifiers | | |
| FT | Region | 53..57 | | |
| FT | | /label= CDR | | |
| FT | Region | /note= "Complementarity determining region" | | |
| FT | | 72..88 | | |
| FT | | /label= CDR | | |
| FT | Region | /note= "Complementarity determining region" | | |
| FT | | 121..126 | | |
| FT | | /label= CDR | | |
| FT | Peptide | /note= "Complementarity determining region" | | |
| FT | | 138..152 | | |
| FT | | /label= Synthetic peptide linker | | |
| FT | Region | /note= "links the heavy chain to the light chain" | | |
| FT | | 176..186 | | |
| FT | | /label= CDR | | |
| FT | Region | /note= "Complementarity determining region" | | |
| FT | | 202..208 | | |
| FT | | /label= CDR | | |
| FT | Region | /note= "Complementarity determining region" | | |
| FT | | 241..249 | | |
| FT | | /label= CDR | | |
| FT | Region | /note= "Complementarity determining region" | | |

| | | |
|----------|---|-----------------------------------|
| FT | Region | 260..267 |
| FT | /label= Glu_Glu_epitope | |
| XX | | |
| XX | WO200153354-A2. | |
| PN | | |
| PD | 26-JUL-2001. | |
| XX | | |
| XX | | |
| PF | 19-JAN-2001; 2001MO-US001919. | |
| XX | | |
| PR | 20-JAN-2000; 2000US-0177258P. | |
| XX | | |
| XX | (CHIR) CHIRON CORP. | |
| PA | (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC. | |
| PA | (HAMI-) HAMILTON REGIONAL CANCER CENTR. | |
| XX | | |
| PI | Austin R, Kwok CS, Ring DB; | |
| XX | | |
| DR | WPI, 2001-451904/48. | |
| DR | N-PSDB; AAS09507. | |
| PT | | |
| PT | Novel immunoconjugate useful for inhibiting tumor cell growth in vivo | |
| PT | comprises a humanized anti-p185 antibody linked to an Interleukin-2 | |
| PT | polypeptide. | |
| XX | | |
| PS | Claim 7; Fig 9; 74pp; English. | |
| CC | | |
| CC | The sequence represents a humanised anti-p185 single chain antibody which | |
| CC | is linked to a human interleukin-2 (IL-2) molecule to make a fusion | |
| CC | protein. The fusion protein (or immunoconjugate) is used to inhibit the | |
| CC | growth of tumours or cancers particularly those characterised by | |
| CC | overexpression of p185 e.g. human adenocarcinomas and malignant and/or | |
| CC | benign tumours of the breast, renal system, salivary gland, | |
| CC | gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to | |
| XX | correct OS field.) | |
| XX | | |
| SQ | Sequence 267 AA; | |
| OY | | |
| Db | 1 WINTYTGSTYADDFKE 17 72 WINTYTGSTYADDFKE 88 | |
| RESULT 8 | | |
| ID | AAU04945 | |
| AC | AAU04945 standard; protein; 409 AA. | |
| XX | | |
| XX | AAU04945; | |
| DT | 06-AUG-2003 (revised) | |
| DT | 24-OCT-2001 (first entry) | |
| DE | | |
| XX | Humanised anti-p185 antibody/IL-2 fusion protein. | |
| XX | | |
| KM | Humanised antibody; p185; 520CGH; interleukin-2; IL-2; immunoconjugate; | |
| RW | cancer; tumour; adenocarcinoma; fusion protein. | |
| XX | | |
| OS | Homo sapiens. | |
| OS | Mus sp. | |
| OS | Synthetic. | |
| OS | Chimeric. | |
| XX | | |
| FT | Key | Location/Qualifiers |
| FT | Peptide | 1..22 |
| FT | Protein | /label= Signal_peptide |
| FT | | 23..409 |
| FT | Protein | /label= Mature_fusion_protein |
| FT | | 23..259 |
| FT | | /label= Humanised_antibody_520CGH |
| FT | Region | 53..57 |


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PT /label= CDR
PT /note= "Complementarity determining region"
PT Region
PT /label= CDR
PT /note= "Complementarity determining region"
PT Region
PT /label= CDR
PT /note= "Complementarity determining region"
PT Misc-difference 123
PT /note= "Encoded by GGG"
PT Peptide
PT /label= Synthetic peptide linker
PT /note= "links the heavy chain to the light chain"
PT Region
PT /label= CDR
PT /note= "Complementarity determining region"
PT Region
PT /label= CDR
PT /note= "Complementarity determining region"
PT Region
PT /label= CDR
PT /note= "Complementarity determining region"
PT Peptide
PT /label= Synthetic linker peptide
PT /note= "links the antibody to the IL-2 molecule"
PT Protein
PT /label= IL_2
PT Misc-difference 406
PT /note= "Encode by ACA"
PT WO200153354-A2.
PT 26-JUL-2001.
PT 19-JAN-2001; 2001WO-US001919.
PT 20-JAN-2000; 2000US-0177258P.
PT (CHAR ) CHIRON CORP.
PT (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PT (HAMI-) HAMILTON REGIONAL CANCER CENT.
PT Austin R, Kwok CS, Ring DB;
PT WPI, 2001-451904/48.
PT DR N-PSDB; AAS09508.
PT Novel immunconjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an Interleukin-2
PT polypeptide.
PT Claim 13; Fig 11; 74pp; English.
XX
XX The sequence represents a humanised anti-p185 (520C9) single chain
XX antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein
XX (or immunconjugate) is used to inhibit the growth of tumours or cancers
XX particularly those characterised by overexpression of p185 e.g. human
XX adenocarcinomas and malignant and/or benign tumours of the breast, renal
XX system, salivary gland, gastrointestinal tract or gastric tumours.
XX (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 409 AA;
Query Match 100.0%; Score 97; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WINTYGOSTYADDFKE 17
DB 72 WINTYGOSTYADDFKE 88

```

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AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
XX AAR39571;
AC AAR39571;
XX
XX 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
XX Sequence of G-FIT.
DE
XX
XX Tumour antigen; c-erbB-2; G-FIT.
XX
XX Synthetic.
OS
XX
XX WO9316185-A2.
XX
XX 19-AUG-1993.
XX
XX 05-FEB-1993; 93WO-US001055.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX (CERTU ) CERTUS ONCOLOGY CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX WPI, 1993-272889/34.
XX DR N-PSDB; AAQ46086.
XX
XX New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
XX imaging or treating breast or ovarian cancer etc.
XX
XX Example; Page 65-68; 87pp; English.
XX
XX c-erbB-2 refers to a protein antigen expressed on the surface of tumour
XX cells, such as breast and ovarian tumour cells, which is an approx.
XX 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
XX 5.3 (see AAQ46083, AAR39568). (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
SQ Sequence 534 AA;
Query Match 100.0%; Score 97; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WINTYGOSTYADDFKE 17
DB 339 WINTYGOSTYADDFKE 355

```

```

RESULT 10
AAB28159
ID AAB28159 standard; protein; 253 AA.
XX
XX AAB28159;
AC AAB28159;
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Murine anti-BGP-2 single chain Fv fragment.
DE
XX
XX Murine; immunoglobulin; antigen-binding; framework region; carcinoma;
XX c-erbB2; carcinoma-associated antigen.
XX
XX Mus sp.
XX
XX WO200061635-A2.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-EP003176.
XX

```

PR 09-APR-1999; 99EP-00107030.
 XX (UYZU-) UNIV ZUERICH.
 PA (PLUE/) PLUECKTHUN A.
 XX PI Plueckthun A, Honegger A, Willuda J;
 XX WPI; 2000-679468/66.
 DR Stabilizing chimeric immunoglobulin (Ig) involves setting up a stabilized
 XX antigen binding Ig or its fragment by replacing one or more residues
 PT present in acceptor Ig by those residues present in donor Ig.
 XX
 PS Claim 6; Page 51; 51pp; English.
 XX
 CC The present invention relates to a method for stabilising a chimeric
 CC immunoglobulin (Ig). The method comprises identifying antigen-binding
 CC groups derived from donor Ig and framework regions derived from an
 CC acceptor Ig. The present sequence is one such donor Ig fragment. One or
 CC more of the residues present at the positions in the present sequence are
 CC replaced by those present at the corresponding positions in the donor Ig,
 CC after comparing the structural features of the VH domains of the acceptor
 CC Ig and the donor Ig. The acceptor Ig fragment used in the present
 CC invention is human anti-c-erbB2 single chain Fv fragment 4D5 (AA028158).
 CC The method of the present invention is useful for producing a
 CC pharmaceutical composition which can be used for treating human
 CC carcinomas, since c-erbB2 is a carcinoma-associated antigen
 XX
 SQ Sequence 253 AA;
 XX
 Query Match 91.8%; Score 89; DB 3; Length 253;
 Best Local Similarity 93.8%; Pred. No. 1.9e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WINTYTGSTYADDFK 16
 DB 187 WINTYTGSTYADDFK 202
 XX
 RESULT 11
 AAW35131
 ID AAW35131 standard; protein; 365 AA.
 XX
 AC AAW35131;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE R. pipiens recombinant RNase ronc fusion protein 7.
 XX
 KW RNase A; ribonuclease; cytotoxic; onconase; ronc; immunofusion;
 KW tumour cell growth; frog.
 XX
 OS Rana pipiens.
 OS Synthetic.
 OS
 PN WO9731116-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 19-FEB-1997; 97WO-US002588.
 XX
 PR 21-FEB-1996; 96US-0011800P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL, Bogue L, Wlodawer A;
 XX WPI; 1997-435168/40.
 DR N-PSDB; AAT94969.
 XX
 PT Ribonuclease molecules based on native Onconase - used for killing cells,
 PT particularly tumour cells.
 XX

PS Disclosure; Page 73; 90pp; English.
 XX
 CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
 CC (ronc) which are modifications of the RNase Onconase (RTM) (ronc). Such
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone
 CC or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 CC also be used for cell separation in vitro by selectively killing unwanted
 CC types of cells, e.g. in bone marrow prior to transplantation into a
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia
 CC cells or T-cells that would cause graft versus host disease. The toxins
 CC can also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to ronc and also
 CC lower immunogenicity in humans
 XX
 SQ Sequence 365 AA;
 XX
 Query Match 91.8%; Score 89; DB 2; Length 365;
 Best Local Similarity 93.8%; Pred. No. 2.9e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WINTYTGSTYADDFK 16
 DB 168 WINTYTGSTYADDFK 183
 XX
 RESULT 12
 AAW35132
 ID AAW35132 standard; protein; 366 AA.
 XX
 AC AAW35132;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE R. pipiens recombinant RNase ronc fusion protein 8.
 XX
 KW RNase A; ribonuclease; cytotoxic; onconase; ronc; immunofusion;
 KW tumour cell growth; frog.
 XX
 OS Rana pipiens.
 OS Synthetic.
 OS
 PN WO9731116-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 19-FEB-1997; 97WO-US002588.
 XX
 PR 21-FEB-1996; 96US-0011800P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL, Bogue L, Wlodawer A;
 XX WPI; 1997-435168/40.
 DR N-PSDB; AAT94970.
 XX
 PT Ribonuclease molecules based on native Onconase - used for killing cells,
 PT particularly tumour cells.
 XX
 PS Disclosure; Page 74; 90pp; English.
 XX
 CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
 CC (ronc) which are modifications of the RNase Onconase (RTM) (ronc). Such
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone
 CC or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 CC also be used for cell separation in vitro by selectively killing unwanted
 CC types of cells, e.g. in bone marrow prior to transplantation into a
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia
 CC cells or T-cells that would cause graft versus host disease. The toxins
 CC can also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to ronc and also

| | |
|----------|--|
| CC | lower immunogenicity in humans |
| XX | |
| SQ | Sequence 366 AA; |
| | Query Match 91.8%; Score 89; DB 2; length 366; Best Local Similarity 93.8%; Pred. No. 2,9e-05; Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0. |
| Oy | 1 WINTYTGOSTYADDPK 16 : |
| Db | 51 WINTYTGESTYADDPK 66 |
| | RESULT 13 |
| AAp70625 | |
| ID | AAp70625 standard; protein; 183 AA. |
| XX | |
| AC | AAp70625; |
| XX | |
| DT | 03-OCT-2002 (revised) |
| DT | 09-APR-1991 (first entry) |
| XX | |
| DE | Sequence encoded by the V region of the L6 VH CDNA clone p13-6a. |
| KM | Chimeric antibody; Anti-cancer antibody. |
| XX | |
| OS | Mue sp. |
| XX | |
| FH | Key |
| FT | Region |
| FT | Location/Qualifiers 1..19 |
| FT | /*tag= a |
| FT | /label= leader peptide |
| FT | 20..49 |
| FT | /*tag= b |
| FT | /label= FR1 |
| FT | 50..54 |
| FT | /*tag= c |
| FT | /label= CDR1 |
| FT | 55..68 |
| FT | /*tag= d |
| FT | /label= FR2 |
| FT | 69..85 |
| FT | /*tag= e |
| FT | /label= CDR2 |
| FT | 86..117 |
| FT | /*tag= f |
| FT | /label= FR3 |
| FT | 118..124 |
| FT | /*tag= g |
| FT | /label= CDR3 |
| FT | 125..139 |
| FT | /*tag= h |
| FT | /label= JH2 |
| FT | 129..139 |
| FT | /*tag= i |
| FT | /label= FR4 |
| FT | 140..183 |
| FT | /*tag= j |
| FT | /label= C12a |
| XX | |
| PN | W08702671-A. |
| XX | |
| PD | 07-MAY-1987. |
| XX | |
| PF | 27-OCT-1986; 86WO-US002269. |
| XX | |
| PR | 01-NOV-1985; 85US-00793980. |
| XX | |
| PA | (ITGE-) INT GENETIC ENG INC. |
| PA | (ROBI/) ROBINSON R R. |
| PI | Robinson RR, Liu AY, Horwitz AH, Wall R; |
| XX | |

| | |
|---|---|
| | WP1_1987-136004/19. |
| DR | N-PsDB; AAN70969. |
| XX | |
| PT | Prodn. of immunoglobulin chains and molecules - is by recombinant DNA |
| PT | procedures, with chimeric antibodies etc. related to cancer specific |
| PT | antigens. |
| XX | |
| PS | Example; Fig 15; 126pp; English. |
| XX | |
| CC | The patentors claim a chimeric antibody molecule comprising 2 light |
| CC | chains and 2 heavy chains, each comprising a constant human region and a |
| CC | variable non-human region. Coding sequences for the Ig chains are also |
| CC | claimed. The invention provides consensus sequences of light and heavy |
| CC | chain J regions useful in the design of oligonucleotides (UGs) for use |
| CC | as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs |
| CC | or genes. Depending on the nature of design of a particular UG, it may |
| CC | be capable of hybridizing to all Ig mRNAs or genes containing a single |
| CC | specific J sequence. UG denotes universal immunoglobulin gene. (updated |
| CC | on 03-OCT-2002 to add missing OS field.) |
| XX | |
| SQ | Sequence 183 AA; |
| | |
| Query March | 89.7%; Score 87; DB 1; Length 183; |
| Best Local Similarity | 93.8%; Pred. No. 2.8e-05; |
| Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0. | |
| OY | 1 WINTYTGGSTYADDPK 16 69 WINTYTGGPTYADDPK 84 |
| Db | |
| RESULT 14 | |
| AAP82936 | |
| ID | AAP82936 standard; protein; 183 AA. |
| XX | |
| AC | AAP82936; |
| XX | |
| DT | 25-MAR-2003 (revised) |
| DT | 03-OCT-2002 (revised) |
| DT | 12-DEC-1990 (first entry) |
| XX | |
| DE | Variable region of the L6Vh cDNA clone pH3-6a. |
| XX | |
| KW | Mouse immunoglobulin; variable region; tumour antigen; |
| KW | chimeric antibodies; L6Vh; pH3-6a. |
| XX | |
| OS | Mus sp. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | 1..19 |
| FT | /label= leader_peptide |
| FT | 20..49 |
| FT | /label= FR1 |
| FT | 50..54 |
| FT | /label= CDR1 |
| FT | 55..68 |
| FT | /label= FR2 |
| FT | 69..85 |
| FT | /label= CDR2 |
| FT | 86..117 |
| FT | /label= FR3 |
| FT | 118..128 |
| FT | /label= CDR3 |
| FT | 129..139 |
| FT | /label= Jn2 |
| FT | Region 129..183 |
| FT | /label= FR4 |
| FT | Region 140..183 |
| FT | /label= C gamma 2a |
| XX | |
| FN | WO8803145-A. |
| PD | 05-MAY-1988. |

```

XX PF 27-OCT-1987; 87WO-US002832.
XX PR 27-OCT-1986; 86US-00923244.
XX (ITGE-) INT GENETIC ENG INC.
XX (ONCO ) ONCOGEN.
XX (ONCO ) ONCOGEN.
XX Liu AY, Robinson RR, Hellstrom KE, Hellstrom I;
XX MPI: 1988-133226/19.
XX N-PSDB; AAN82417.
XX
XX PT New polynucleotide encoding variable region of mouse immunoglobulin -
XX PT specific for human tumour antigen, and expression products, including
XX PT complete chimeric human-mouse antibodies.
XX PS Disclosure; Page ?; 83pp; English.
XX
XX A library primed by oligo (dT) on L6 poly (A+) RNA was screened for kappa
XX clones with a mouse Ck region probe. From the L6 library, several clones
XX were isolated. A second screen with a 5' Jk5 specific probe identified
XX the L6 (Jk5) light-chain clones. Heavy chain clones of L6 were isolated
XX be screening with the Jk2 oligonucleotide. The heavy and light chain
XX genes from the clones pH3-6a (and PL3-12a) were inserted into M13
XX bacteriophage vectors of which the sequence was determined by the
XX CC diodeoxyfermentation method. Amino acid residues 26-35 have been confirmed
XX by peptide sequence. See also AAN82415-20. (Updated on 03-OCT-2002 to add
XX missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 183 AA;
XX
XX Query Match 89.7%; Score 87; DB 1; Length 183;
XX Best Local Similarity 93.8%; Pred. No. 2.8e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 WINTYTGSTYADDFK 16
XX |||||||
XX DB 69 WINTYTGPTYADDFK 84
XX
XX RESULT 15
XX ID AAP82938 standard; protein, 183 AA.
XX
XX AC AAP82938;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-OCT-2002 (revised)
XX DT 12-DEC-1990 (first entry)
XX
XX DE Variable region of clone M13mp19-Cl-delta 4 (Cl-delta 4).
XX
XX KM Mouse immunoglobulin; variable region; tumour antigen;
XX KM chimeric antibodies; Bal-31 deletion clone M13mp19-Cl-delta 4.
XX
XX OS Mus sp.
XX
XX FH Key Location/Qualifiers
XX FT 1..19
XX FT /label= leader_peptide
XX FT 20..49
XX FT /label= FR1
XX FT 50..54
XX FT /label= CDRI
XX FT 55..68
XX FT /label= FR2
XX FT 69..85
XX FT /label= CDR2
XX FT 86..117
XX FT /label= FR3
XX FT 118..128

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FT FT /label= CDR3
FT FT 125..139
FT FT /label= Jh2
FT FT 129..183
FT FT /label= FR4
FT FT 140..183
FT FT /label= C gamma 2a
XX
XX PN WO8803145-A.
XX
XX PD 05-MAY-1988.
XX
XX PF 27-OCT-1987; 87WO-US002832.
XX
XX PR 27-OCT-1986; 86US-00923244.
XX
XX PA (ITGE-) INT GENETIC ENG INC.
XX PA (ONCO ) ONCOGEN.
XX PA (ONCO ) ONCOGEN.
XX
XX LIU AY, Robinson RR, Hellstrom KE, Hellstrom I;
XX MPI: 1988-133226/19.
XX N-PSDB; AAN82419.
XX
XX PT New polynucleotide encoding variable region of mouse immunoglobulin -
XX PT specific for human tumour antigen, and expression products, including
XX PT complete chimeric human-mouse antibodies.
XX PS Disclosure; Page ?; 83pp; English.
XX
XX CC The nuclease Bal-31 was used to chew away the oligo (dC) in the L6 Vh
XX CC clone pH3-6a (AAN82417). For this clone nucleotides 1-38 were deleted.
XX CC Then the sequence was modified by site-directed mutagenesis with the MJH2
XX CC -ApaI primer. This 31-base primer introduces an ApaI site in the mouse Ch
XX CC gene at position at a position analogous to human Cgamma1 cDNA gene
XX CC module. See also AAN82415-20. (Updated on 03-OCT-2002 to add missing OS
XX CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 183 AA;
XX
XX Query Match 89.7%; Score 87; DB 1; Length 183;
XX Best Local Similarity 93.8%; Pred. No. 2.8e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 WINTYTGSTYADDFK 16
XX |||||||
XX DB 69 WINTYTGPTYADDFK 84

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Search completed: April 4, 2005, 15:47:08
 Job time : 34.9457 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 25.0927 seconds

(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_50_66

Perfect score: 97

Sequence: 1 WINTYTGSTADDFKE 17

Scoring table: BLOSUM62

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Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 97 | 100.0 | 243 | 9 | US-09-887-853-6 |
| 2 | 97 | 100.0 | 243 | 17 | US-10-683-547-6 |
| 3 | 97 | 100.0 | 267 | 9 | US-09-766-543-10 |
| 4 | 97 | 100.0 | 276 | 9 | US-09-766-543-12 |
| 5 | 89 | 91.8 | 116 | 9 | US-09-971-543-8 |
| 6 | 89 | 91.8 | 253 | 9 | US-09-971-543-2 |
| 7 | 85 | 87.6 | 230 | 14 | US-10-071-485-102 |
| 8 | 85 | 87.6 | 235 | 14 | US-10-071-485-93 |
| 9 | 85 | 87.6 | 240 | 14 | US-10-071-485-91 |
| 10 | 85 | 87.6 | 267 | 14 | US-10-071-485-2 |
| 11 | 85 | 87.6 | 468 | 14 | US-10-071-485-67 |
| 12 | 85 | 87.6 | 541 | 14 | US-10-071-485-85 |
| 13 | 85 | 87.6 | 711 | 14 | US-10-071-485-90 |

| | | | | | | |
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| 14 | 84 | 86.6 | 17 | 10 | US-09-791-551-86 | Sequence 86, App1 |
| 15 | 84 | 86.6 | 17 | 16 | US-10-018-245A-2 | Sequence 2, App1 |
| 16 | 84 | 86.6 | 17 | 16 | US-10-467-253-5 | Sequence 5, App1 |
| 17 | 84 | 86.6 | 67 | 14 | US-10-243-130-19 | Sequence 19, App1 |
| 18 | 84 | 86.6 | 70 | 14 | US-10-243-130-17 | Sequence 17, App1 |
| 19 | 84 | 86.6 | 70 | 14 | US-10-243-130-18 | Sequence 18, App1 |
| 20 | 84 | 86.6 | 70 | 17 | US-10-901-650-17 | Sequence 17, App1 |
| 21 | 84 | 86.6 | 70 | 17 | US-10-901-650-18 | Sequence 18, App1 |
| 22 | 84 | 86.6 | 70 | 17 | US-10-901-650-19 | Sequence 19, App1 |
| 23 | 84 | 86.6 | 112 | 15 | US-10-383-447-10 | Sequence 10, App1 |
| 24 | 84 | 86.6 | 112 | 15 | US-10-383-447-18 | Sequence 18, App1 |
| 25 | 84 | 86.6 | 116 | 14 | US-10-138-727A-2 | Sequence 2, App1 |
| 26 | 84 | 86.6 | 116 | 14 | US-10-138-727A-18 | Sequence 18, App1 |
| 27 | 84 | 86.6 | 116 | 14 | US-10-138-727A-19 | Sequence 19, App1 |
| 28 | 84 | 86.6 | 116 | 14 | US-10-138-727A-20 | Sequence 20, App1 |
| 29 | 84 | 86.6 | 116 | 14 | US-10-138-727A-21 | Sequence 21, App1 |
| 30 | 84 | 86.6 | 116 | 14 | US-10-138-727A-22 | Sequence 22, App1 |
| 31 | 84 | 86.6 | 116 | 14 | US-10-138-727A-23 | Sequence 23, App1 |
| 32 | 84 | 86.6 | 116 | 14 | US-10-138-727A-24 | Sequence 24, App1 |
| 33 | 84 | 86.6 | 116 | 14 | US-10-138-727A-25 | Sequence 25, App1 |
| 34 | 84 | 86.6 | 116 | 14 | US-10-138-727A-26 | Sequence 26, App1 |
| 35 | 84 | 86.6 | 116 | 14 | US-10-310-719-30 | Sequence 30, App1 |
| 36 | 84 | 86.6 | 116 | 14 | US-10-310-719-33 | Sequence 33, App1 |
| 37 | 84 | 86.6 | 116 | 15 | US-10-468-370-658 | Sequence 658, App |
| 38 | 84 | 86.6 | 116 | 15 | US-10-468-370-660 | Sequence 660, App |
| 39 | 84 | 86.6 | 116 | 15 | US-10-468-370-662 | Sequence 662, App |
| 40 | 84 | 86.6 | 116 | 15 | US-10-468-370-664 | Sequence 664, App |
| 41 | 84 | 86.6 | 116 | 15 | US-10-468-370-666 | Sequence 666, App |
| 42 | 84 | 86.6 | 116 | 15 | US-10-468-370-668 | Sequence 668, App |
| 43 | 84 | 86.6 | 116 | 15 | US-10-468-370-670 | Sequence 670, App |
| 44 | 84 | 86.6 | 116 | 15 | US-10-468-370-672 | Sequence 672, App |
| 45 | 84 | 86.6 | 116 | 16 | US-10-468-496-2021 | Sequence 2021, App |

ALIGNMENTS

RESULT 1

US-09-887-853-6

Sequence 6, Application US/09887853

Patent No. US20020168375A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

Oppermann, Hermann

Houston, L. L.

Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: Teetla, Hurwitz & Thibault/Patent Department

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 100.0%; Score 97; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||||
DB 50 WINTYTGSTYADDFKE 66

RESULT 2
US-10-683-547-6
Sequence 6, Application US/10683547
Publication No. US20050058638A1
GENERAL INFORMATION:
APPLICANT: Houston, J.
APPLICANT: Houston, L.L.
APPLICANT: Ring, D.
APPLICANT: Oppertmann, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: CIBR-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 07/831,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 520c9 sfv
US-10-683-547-6

Query Match 100.0%; Score 97; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||||
DB 50 WINTYTGSTYADDFKE 66

RESULT 3
US-09-766-543-10
Sequence 10, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: P01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/177,258
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10

LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 520C9
OTHER INFORMATION: humanized single-chain antibody used in the
OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 100.0%; Score 97; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||||
DB 72 WINTYTGSTYADDFKE 88

RESULT 4
US-09-766-543-12
Sequence 12, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: P01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/177,258
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
OTHER INFORMATION: linker
US-09-766-543-12

Query Match 100.0%; Score 97; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
|||||
DB 72 WINTYTGSTYADDFKE 88

RESULT 5
US-09-971-543-8
Sequence 8, Application US/09971543
Patent No. US20020146846A1
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HONEGGER, ANNEMARIE
APPLICANT: WILDHA, JORG
TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC
TITLE OF INVENTION: IMMUNOGLOBULINS OR IMMUNOGLOBULIN FRAGMENTS, AND
TITLE OF INVENTION: STABILIZED ANTI-BGP-2 scfv FRAGMENT
FILE REFERENCE: PLUCK-3 CON
CURRENT APPLICATION NUMBER: US/09/971,543
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: PCT/EP00/03176
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: EP 99 10 7030.1
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8

LENGTH: 116
TYPE: PRT
ORGANISM: Mus sp.
US-09-971-543-8

Query Match
Beet Local Similarity 91.8%; Score 89; DB 9; Length 116;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGOSTYADDFK 16
Db 50 WINTYGESTYADDFK 65

RESULT 6
US-09-971-543-2

Sequence 2, Application US/09971543
Patent No. US20020146846A1

GENERAL INFORMATION:

APPLICANT: PLUCKTHUN, ANDREAS

APPLICANT: HONEGGER, ANNEMARIE

APPLICANT: WILUDA, JORG

TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHIMERIC

TITLE OF INVENTION: IMMUNOGLOBULINS OR IMMUNOGLOBULIN FRAGMENTS, AND

TITLE OF INVENTION: STABILIZED ANTI-EGF-2 scfv FRAGMENT

FILE REFERENCE: PLUCK-3 CON

CURRENT APPLICATION NUMBER: US/09/971,543

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: PCT/EP00/03176

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: EP 99 10 7030.1

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 253

TYPE: PRT

ORGANISM: Mus sp.

US-09-971-543-2

Query Match
Beet Local Similarity 91.8%; Score 89; DB 9; Length 253;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGOSTYADDFK 16
Db 187 WINTYGESTYADDFK 202

RESULT 7
US-10-071-485-102

Sequence 102, Application US/10071485

Publication No. US20030099648A1

GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange

APPLICANT: Sablon, Erwin

TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/10/071,485

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/EP 98/05165

PRIOR FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: EPO 98870139.7

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: EPO 97870122.5

PRIOR FILING DATE: 1997-08-18

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn version 3.0

SEQ ID NO 102

LENGTH: 230
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC
US-10-071-485-102

Query Match
Beet Local Similarity 87.6%; Score 85; DB 14; Length 230;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGOSTYADDFK 16
Db 50 WINTYGESTYADDFK 65

RESULT 8
US-10-071-485-93

Sequence 93, Application US/10071485

Publication No. US20030099648A1

GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange

APPLICANT: Sablon, Erwin

TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/10/071,485

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/EP 98/05165

PRIOR FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: EPO 98870139.7

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: EPO 97870122.5

PRIOR FILING DATE: 1997-08-18

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn version 3.0

SEQ ID NO 93

LENGTH: 235

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: SYNTHETIC
US-10-071-485-93

Query Match
Beet Local Similarity 87.6%; Score 85; DB 14; Length 235;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGOSTYADDFK 16
Db 50 WINTYGESTYADDFK 65

RESULT 9
US-10-071-485-91

Sequence 91, Application US/10071485

Publication No. US20030099648A1

GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange

APPLICANT: Sablon, Erwin

TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/10/071,485

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/EP 98/05165

PRIOR FILING DATE: 1998-08-14

```

; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-91
```

```

Query Match      87.6%; Score 85; DB 14; Length 240;
Best Local Similarity 87.5%; Pred. No. 2,6e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYTGSTYADDFK 16
         |||||:|||||
Db      50 WINTYTGSTYVDDFK 65
```

```

RESULT 10
US-10-071-485-2
; Sequence 2, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-071-485-2
```

```

Query Match      87.6%; Score 85; DB 14; Length 267;
Best Local Similarity 87.5%; Pred. No. 2,9e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYTGSTYADDFK 16
         |||||:|||||
Db      72 WINTYTGSTYVDDFK 87
```

```

RESULT 11
US-10-071-485-67
; Sequence 67, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
```

```

; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67
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```

Query Match      87.6%; Score 85; DB 14; Length 468;
Best Local Similarity 87.5%; Pred. No. 5,1e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYTGSTYADDFK 16
         |||||:|||||
Db      70 WINTYTGSTYVDDFK 85
```

```

RESULT 12
US-10-071-485-85
; Sequence 85, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-85
```

```

Query Match      87.6%; Score 85; DB 14; Length 541;
Best Local Similarity 87.5%; Pred. No. 5,9e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYTGSTYADDFK 16
         |||||:|||||
Db      50 WINTYTGSTYVDDFK 65
```

```

RESULT 13
US-10-071-485-90
; Sequence 90, Application US/10071485
```



```
/ Publication No. US20030099648A1
/ GENERAL INFORMATION:
/ APPLICANT: Buyse, Marie-Ange
/ APPLICANT: Sablon, Edwin
/ TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
/ TITLE OF INVENTION: SHOCK
/ FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
/ CURRENT APPLICATION NUMBER: US/10/071,485
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 09/485,737
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: PCT/EP 98/05165
/ PRIOR FILING DATE: 1998-08-14
/ PRIOR APPLICATION NUMBER: EPO 98870139.7
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: EPO 97870122.5
/ PRIOR FILING DATE: 1997-08-18
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 90
/ LENGTH: 711
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC
US-10-071-485-90
```

```
Query Match      87.6%; Score 85; DB 14; Length 711;
Best Local Similarity 87.5%; Pred. No. 7.8e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGOSTYADDFK 16
DB      70 WINTYTGSEPTYADDFK 85
```

```
RESULT 14
US-09-791-551-86
/ Sequence 86, Application US/09791551
/ Publication No. US20030235584A1
/ GENERAL INFORMATION:
/ APPLICANT: KLOETZER, WILLIAM S.
/ APPLICANT: HANNA, NABIL
/ TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
/ FILE REFERENCE: 03/7003/0277869
/ CURRENT APPLICATION NUMBER: US/09/791,551
/ CURRENT FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 60/185,390
/ PRIOR FILING DATE: 2000-02-28
/ PRIOR APPLICATION NUMBER: 60/233,625
/ PRIOR FILING DATE: 2000-09-18
/ NUMBER OF SEQ ID NOS: 119
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 86
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Mus sp.
US-09-791-551-86
```

```
Query Match      86.6%; Score 84; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGOSTYADDFK 16
DB      1 WINTYTGSEPTYADDFK 16
```

```
RESULT 15
US-10-018-245A-2
/ Sequence 2, Application US/10018245A
/ Publication No. US20040115196A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: FUKUDA, Yoshiaki
/ APPLICANT: NAGAHIRA, Kazuhiro
/ APPLICANT: NAKANISHI, Toshihiro
/ TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
/ TITLE OF INVENTION: determining regions and genes encoding the same
/ FILE REFERENCE: 46224
/ CURRENT APPLICATION NUMBER: US/10/018,245A
/ CURRENT FILING DATE: 2002-07-12
/ PRIOR APPLICATION NUMBER: JP 117394/2000
/ PRIOR FILING DATE: 2000-04-19
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: mouse
/ FEATURE:
/ OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
US-10-018-245A-2
```

```
Query Match      86.6%; Score 84; DB 16; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYGOSTYADDFK 16
DB      1 WINTYTGSEPTYADDFK 16
```

```
Search completed: April 4, 2005, 16:42:44
Job time : 26.0927 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 6.13738 Seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_50_66

Perfect score: 97

Sequence: 1 WINTYTGQSTYADDFKE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:79:*
2: PIR:1:*
3: PIR:3:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 87 | 89.7 | 115 | 2 | SI9968 |
| 2 | 87 | 89.7 | 120 | 2 | B42848 |
| 3 | 87 | 89.7 | 146 | 4 | S33905 |
| 4 | 85 | 87.6 | 136 | 2 | S35759 |
| 5 | 84 | 86.6 | 101 | 2 | D24672 |
| 6 | 84 | 86.6 | 105 | 2 | S24764 |
| 7 | 84 | 86.6 | 105 | 2 | S24765 |
| 8 | 84 | 86.6 | 109 | 2 | S26325 |
| 9 | 84 | 86.6 | 118 | 2 | SI9967 |
| 10 | 84 | 86.6 | 119 | 2 | A53285 |
| 11 | 84 | 86.5 | 124 | 2 | PH1404 |
| 12 | 80 | 82.5 | 102 | 2 | C32530 |
| 13 | 79 | 81.4 | 115 | 2 | SI9965 |
| 14 | 76 | 78.4 | 114 | 2 | D32967 |
| 15 | 76 | 78.4 | 114 | 2 | C32967 |
| 16 | 76 | 78.4 | 117 | 2 | S33187 |
| 17 | 76 | 78.4 | 117 | 2 | S33190 |
| 18 | 75 | 77.3 | 105 | 2 | S24766 |
| 19 | 75 | 77.3 | 113 | 2 | B36259 |
| 20 | 74 | 76.3 | 118 | 2 | A32530 |
| 21 | 74 | 76.3 | 119 | 2 | B32530 |
| 22 | 71 | 73.2 | 118 | 2 | S37204 |
| 23 | 70 | 72.2 | 120 | 2 | SI9963 |
| 24 | 70 | 72.2 | 139 | 2 | PH1225 |
| 25 | 69.5 | 71.6 | 119 | 2 | H45722 |
| 26 | 69 | 71.1 | 114 | 2 | PL0256 |
| 27 | 67 | 69.1 | 93 | 2 | C24672 |
| 28 | 67 | 69.1 | 99 | 2 | S26326 |
| 29 | 62 | 63.9 | 120 | 2 | S26789 |

| | | | | | | |
|----|------|------|-----|---|--------|--------------------|
| 30 | 60 | 61.9 | 98 | 2 | S46460 | Ig heavy chain V r |
| 31 | 57 | 58.8 | 134 | 2 | S21916 | Ig heavy chain V r |
| 32 | 56 | 57.7 | 105 | 2 | S24763 | Ig heavy chain V r |
| 33 | 55 | 56.7 | 98 | 2 | A49051 | Ig heavy chain V r |
| 34 | 55 | 56.7 | 117 | 2 | SI8554 | Ig heavy chain V r |
| 35 | 55 | 56.7 | 131 | 2 | S26792 | Ig heavy chain V r |
| 36 | 54 | 55.7 | 446 | 2 | S67437 | Damage and replica |
| 37 | 51 | 52.6 | 142 | 2 | SI9245 | Ig heavy chain pre |
| 38 | 50 | 51.5 | 98 | 2 | H34964 | Ig heavy chain V-I |
| 39 | 47 | 48.5 | 367 | 2 | T26291 | hypothetical prote |
| 40 | 46 | 47.4 | 215 | 2 | T27462 | hypothetical prote |
| 41 | 46 | 47.4 | 349 | 2 | AF2130 | iron(III) diclrat |
| 42 | 45 | 46.4 | 122 | 2 | PH0887 | Ig heavy chain V r |
| 43 | 45 | 46.4 | 125 | 2 | E81192 | hypothetical prote |
| 44 | 45 | 46.4 | 209 | 2 | AC0273 | probable exported |
| 45 | 44.5 | 45.9 | 324 | 2 | A86839 | conserved hypotet |

ALIGNMENTS

RESULT 1

SI9968 Ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: SI9968

R.Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: SI9963

A/Accession: SI9968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 <WEI>

A/Cross-references: UNIPROT:0921A6; EMBL:X65089

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 87; DB 2; Length 115;

Best Local Similarity 93.8%; Pred. No. 7.4e-07;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGQSTYADDFK 16

Db 45 WINTYTGQSTYADDFK 60

|||||

RESULT 2

B42848 L6 mAb heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: B42848; S33903

R.Fell, H.P.; Gayle, W.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,

J. Biol. Chem. 267, 15552-15558, 1992

A/Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character;

A/Reference number: A42848; MUID:92348410; PMID:1639794

A/Accession: B42848

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-120 <FEU>

A/Cross-references: GB:M90690; NID:9195065; PID:AAA38146.1; PID:9195066

A/Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)

A/Accession: S33903

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <FE2>

C/Cross-references: EMBL:M90691

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 87; DB 2; Length 120;
Best Local Similarity 93.8%; Pred. No. 7.8e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 50 WINTYTGOPYADDFK 65

RESULT 3

Ig heavy chain precursor V region - synthetic

C/Species: synthetic
C/Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
C/Accession: S33905
R; Liu, A.Y.; Robinson, R.R.; Hellestroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellestroem
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987
A/Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.
A/Reference number: S33905; MUID:87204152; PMID:3306970
A/Accession: S33905
A/Molecule type: mRNA
A/Residues: 1-146 <LIT>
A/Cross-references: EMBL:MA6072; NID:G195270; PID:AAA38229.1; PID:G195271

Query Match 89.7%; Score 87; DB 4; Length 146;
Best Local Similarity 93.8%; Pred. No. 9.6e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 69 WINTYTGOPYADDFK 84

RESULT 4

BHPD10 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S35759
R; Kroym, G.F.V.
Submitted to the EMBL Data Library, May 1993
A/Reference number: S35759
A/Accession: S35759
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-136 <PRO>
A/Cross-references: EMBL:X72796; NID:G312496; PID:CAA53316.1; PID:G312497
C/Superfamily: immunoglobulin V region; immunoglobulin homology
P;34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 85; DB 2; Length 136;
Best Local Similarity 87.5%; Pred. No. 1.9e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 69 WINTYTGESTYADDFK 84

RESULT 5

Ig heavy chain V region (VGA3-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C/Accession: D24672
R; Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A/Reference number: A91022; MUID:86055722; PMID:2998759
A/Accession: D24672
A/Molecule type: DNA
A/Residues: 1-101 <WIN>
A/Cross-references: GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G773215
A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 101;
Best Local Similarity 87.5%; Pred. No. 2e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 31 WINTYTGEPYADDFK 46

RESULT 6

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C/Accession: S24764; S24772; S24777
R; Klages, S.
Submitted to the EMBL Data Library, August 1992
A/Reference number: S24763
A/Accession: S24764
A/Molecule type: DNA
A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z14999
A/Accession: S24772
A/Molecule type: DNA
A/Residues: 1-105 <KLM>
A/Cross-references: EMBL:Z15011
R; Thomas, J.W.
Submitted to the EMBL Data Library, August 1992
A/Reference number: S24776
A/Accession: S24777
A/Molecule type: DNA
A/Residues: 1-105 <THO>
A/Cross-references: EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:G52617
C/Genetics:
A/Introns: 9/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 105;
Best Local Similarity 87.5%; Pred. No. 2.1e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGOSTYADDFK 16
|||||:|||||
Db 62 WINTYTGEPYADDFK 77

RESULT 7

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C/Accession: S24765; S24773; S24778
R; Klages, S.
Submitted to the EMBL Data Library, August 1992
A/Reference number: S24763
A/Accession: S24765
A/Molecule type: DNA
A/Residues: 1-105 <KLA>
A/Cross-references: EMBL:Z15001
A/Accession: S24773
A/Molecule type: DNA
A/Residues: 1-105 <KLM>
A/Cross-references: EMBL:Z15013
R; Thomas, J.W.
Submitted to the EMBL Data Library, August 1992
A/Reference number: S24776
A/Accession: S24778
A/Molecule type: DNA
A/Residues: 1-105 <THO>

A:Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620
C:Genetics:
A:Introns: 9/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.6%; Score 84; DB 2; Length 105;
Best Local Similarity 87.5%; Pred. No. 2.1e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTVADDFK 16
|||||:|||||
DB 62 WINTYTGERTVADDFK 77

RESULT 8
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S26325
R:Stark, S.B.; Caton, A.U.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26325
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:G52080; PID:G1334043
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:5-88/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 109;
Best Local Similarity 87.5%; Pred. No. 2.1e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTVADDFK 16
|||||:|||||
DB 40 WINTYTGERTVADDFK 55

RESULT 9
S19967
Ig heavy chain V region (M-T406) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S19967
R:Weissenborn, W.; Rietmuller, G.; Weis, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mab.
A:Reference number: S19963
A:Accession: S19967
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <WEI>
A:Cross-references: UNIPROT:Q921A6; EMBL:X65090
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 118;
Best Local Similarity 87.5%; Pred. No. 2.3e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTVADDFK 16
|||||:|||||
DB 47 WINTYTGERTVADDFK 62

RESULT 10
A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53285
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.
A:Reference number: A53285; MUID:92017897; PMID:1922102
A:Accession: A53285
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-119 <SAW>
A:Cross-references: GB:D12736; NID:9220595; PIDN:BA02228.1; PID:9220596
A>Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:63299)
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 2.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTVADDFK 16
|||||:|||||
DB 50 WINTYTGERTVADDFK 65

RESULT 11
PH1404
Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C:Accession: PH1404; PH1406
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Taji, T.
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in the virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1404
A:Molecule type: DNA
A:Residues: 1-124 <SHI>
A:Accession: PH1406
A:Molecule type: DNA
A:Residues: 115-121 <SH2>
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 84; DB 2; Length 124;
Best Local Similarity 87.5%; Pred. No. 2.5e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGOSTVADDFK 16
|||||:|||||
DB 70 WINTYTGERTVADDFK 85

RESULT 12
C32530
Ig heavy chain V region (10/8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-1996
C:Accession: C32530
R:Deverson, E.; Berék, C.; Tauszig, M.; Feinstein, A.
Eur. J. Immunol. 17, 9-13, 1987
A:Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region
A:Reference number: A32530; MUID:87133855; PMID:3102254
A:Accession: C32530
A:Status: preliminary
A:Molecule type: mRNA

A;Residues: 1-102 <DEV>
 A;Cross-references: GB:M27585
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 82.5%; Score 80; DB 2; Length 102;
 Best Local Similarity 81.2%; Pred. No. 8.9e-06;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16
 |||||:|||||
 Db 33 WINTYGTETTYDDFK 48

RESULT 13

S19965
 Ig heavy chain V region (M-T321) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S19965

R;Weissenborn, W.; Riehmuehler, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19965

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <WEI>

A;Cross-references: UNIPROT:Q921A6; EMBL:X65088

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 79; DB 2; Length 115;
 Best Local Similarity 81.2%; Pred. No. 1.5e-05;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16
 |||||:|||||
 Db 43 WINTYGTETTYANNFK 58

RESULT 14

D32967

Ig heavy chain V region TE32 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000

C;Accession: D32967

R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglistter, J.

Biochemistry 28, 7168-7175, 1989

A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted

A;Reference number: A32967; MUID:90057406; PMID:2819059

A;Accession: D32967

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1-114 <LEV>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 76; DB 2; Length 114;
 Best Local Similarity 81.2%; Pred. No. 4.4e-05;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16
 |||||:|||||
 Db 50 WINTYGVPTTYADDFK 65

RESULT 15

C32967

Ig heavy chain V region TE33 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
 C;Accession: C32967
 R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglistter, J.
 Biochemistry 28, 7168-7175, 1989
 A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted
 A;Reference number: A32967; MUID:90057406; PMID:2819059
 A;Accession: C32967
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: mRNA
 A;Residues: 1-114 <LEV>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 76; DB 2; Length 114;
 Best Local Similarity 81.2%; Pred. No. 4.4e-05;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGQSTYADDFK 16
 |||||:|||||
 Db 50 WINTYGVPTTYADDFK 65

Search completed: April 4, 2005, 15:58:00
 Job time : 6.13738 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 28.7316 Seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_50_66
Perfect score: 97
Sequence: 1 WINTYTGQSTYADDFKE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 84 | 86.6 | 241 | 2 | Q92IA6 mus musculus |
| 2 | 75 | 77.3 | 102 | 2 | Q9JL79 mus musculus |
| 3 | 72 | 74.2 | 140 | 2 | Q65EL3 mus sp. Egl |
| 4 | 70 | 72.2 | 116 | 2 | Q683Y7 mus musculus |
| 5 | 68 | 70.1 | 116 | 2 | Q683Y8 mus musculus |
| 6 | 60 | 61.9 | 125 | 2 | Q991A6 mus musculus |
| 7 | 57 | 58.8 | 218 | 2 | Q925S1 mus musculus |
| 8 | 54 | 55.7 | 446 | 1 | CRB3_SCHPO |
| 9 | 53 | 54.6 | 745 | 2 | Q6L2I9 methanococc |
| 10 | 51 | 52.6 | 759 | 2 | Q8A3F1 bacteroides |
| 11 | 48 | 49.5 | 2009 | 2 | Q7N848 bacteroides |
| 12 | 47 | 48.5 | 367 | 2 | Q7YTM2 caenorhabd |
| 13 | 47 | 48.5 | 500 | 2 | Q6N091 homo sapien |
| 14 | 47 | 48.5 | 573 | 2 | Q8A3Y7 bacteroides |
| 15 | 46 | 47.4 | 2992 | 2 | Q7RDX7 neurospora |
| 16 | 46 | 47.4 | 74 | 2 | Q94152 caenorhabd |
| 17 | 46 | 47.4 | 215 | 2 | Q9NA29 caenorhabd |
| 18 | 46 | 47.4 | 349 | 2 | Q8YTM6 anabaena sp |
| 19 | 46 | 47.4 | 357 | 2 | Q6TDC2 onion Yellio |
| 20 | 46 | 47.4 | 576 | 2 | Q65WZ7 oryza sativ |
| 21 | 46 | 47.4 | 2201 | 2 | Q8GF46 zymomonas m |
| 22 | 45 | 46.4 | 125 | 2 | Q9J517 neisseria m |
| 23 | 45 | 46.4 | 209 | 1 | RNFG_YERPE |
| 24 | 45 | 46.4 | 209 | 1 | Q9J517 neisseria m |
| 25 | 45 | 46.4 | 1085 | 2 | Q66A68 thermotoga |
| 26 | 45 | 46.4 | 1335 | 2 | Q7UD00 rhodospira |
| 27 | 44.5 | 45.9 | 304 | 2 | Q9NXY0 giardia lam |
| 28 | 44.5 | 45.9 | 324 | 2 | Q9CEX1 lactococcus |
| 29 | 44 | 45.4 | 612 | 2 | Q9VTS5 drosophila |
| 30 | 44 | 45.4 | 617 | 2 | Q7RE14 plasmodium |

| | | | | | |
|----|------|------|------|---|--------------------|
| 32 | 44 | 45.4 | 793 | 2 | Q6F9M7 acinetobact |
| 33 | 44 | 45.4 | 1549 | 2 | Q76D19 clostridium |
| 34 | 44 | 45.4 | 2061 | 2 | Q9VUH9 drosophila |
| 35 | 44 | 45.4 | 2103 | 2 | Q7KUL0 drosophila |
| 36 | 43.5 | 44.8 | 434 | 2 | Q913J2 pseudomonas |
| 37 | 43.5 | 44.8 | 578 | 2 | Q96V96 orpomyces |
| 38 | 43 | 44.3 | 173 | 2 | Q959A8 galaxias vu |
| 39 | 43 | 44.3 | 178 | 2 | Q72W90 leptospira |
| 40 | 43 | 44.3 | 178 | 2 | Q8F9Y4 leptospira |
| 41 | 43 | 44.3 | 216 | 2 | Q75H58 oryza sativ |
| 42 | 43 | 44.3 | 216 | 2 | Q87BA4 oryza sativ |
| 43 | 43 | 44.3 | 218 | 2 | Q9PFR0 xylella fas |
| 44 | 43 | 44.3 | 329 | 2 | Q8EUA4 xylella fas |
| 45 | 43 | 44.3 | 347 | 2 | Q98D26 rhizobium 1 |

ALIGNMENTS

```
RESULT 1
ID Q92IA6 PRELIMINARY; PRT; 241 AA.
AC Q92IA6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98170165; Pubmed=9509426;
RX Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BMW.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 86.6%; Score 84; DB 2; Length 241;
Best Local Similarity 87.5%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGQSTYADDFK 16
Db 50 WINTYTGQSTYADDFK 65

RESULT 2
ID Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Makiel S., Liao L., Cunningham M.W., Diamond B.,
RT "Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 77.3%; Score 75; DB 2; Length 102;
Best Local Similarity 81.2%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGGSTYADDFK 16
Db 35 WINTETGPTYADDFK 50

RESULT 3

065ZL3 PRELIMINARY; PRT; 140 AA.
AC 065ZL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tg10H (Fragment).
GN Name=Tg10H;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;
RA Noel D., Bernardi T., Navarro-Tenlon I., Martin M., Martinello J.P.,
RT Ducancel F., Mani J.C., Pau B., Piechaczyk M., Biard-Piechaczyk M.,
RT "Analysis of the individual contributions of immunoglobulin heavy and
light chains to the binding of antigen using cell transfection and
RT plasmon resonance analysis.";
RL J. Immunol. Methods 193:177-187 (1996).
DR EMBL; S82492; AAB37434.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965F43 CRC64;

Query Match 74.2%; Score 72; DB 2; Length 140;
Best Local Similarity 75.0%; Pred. No. 0.00068;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGGSTYADDFK 16
Db 69 WINTESGVPTYADDFK 84

RESULT 4

0683Y7

ID 0683Y7 PRELIMINARY; PRT; 116 AA.
AC 0683Y7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipopolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784033; CAH04483.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12863 MW; 5EC11AD02E911952 CRC64;

Query Match 72.2%; Score 70; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WINTYGGSTYADDFK 16
Db 50 WINTETGPTYADDFK 65

RESULT 5

0683Y8 PRELIMINARY; PRT; 116 AA.
AC 0683Y8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipopolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784032; CAH04482.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12833 MW; C85932C0D843778D CRC64;

Query Match 72.2%; Score 70; DB 2; Length 116;

Best Local Similarity 75.0%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16
Db 50 WINTATGPTYPDDFK 65

RESULT 6

Q99LA6 PRELIMINARY; PRT; 484 AA.
ID Q99LA6; 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;

SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesk S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesk S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Query Match 70.1%; Score 68; DB 2; Length 484;
Best Local Similarity 68.8%; Pred. No. 0.011;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 16
Db 69 WVNITGESVYADDFK 84

RESULT 7

Q6PIL0 PRELIMINARY; PRT; 125 AA.
ID Q6PIL0; 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxId=9606;

SEQUENCE FROM N.A.
RC STRAIN=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesk S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE 125 AA; B76CE434F5A69788 CRC64;

Query Match 61.9%; Score 60; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WINTYTGSTVADDFK 15
Db 69 WVNITGESVYADDFK 83

RESULT 8

Q925S1 PRELIMINARY; PRT; 218 AA.

Q925S1; 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;

SEQUENCE FROM N.A.
RC STRAIN=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesk S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RC STRAIN=BAJB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; 10NZ.
DR SMART; SM00406; IG, 1.
DR PROSITE; PS50835; IG_LIKE, 1.
FT NCN TER 218
FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
SO
Query Match 58.8%; Score 57; DB 2; Length 218;
Best Local Similarity 56.2%; Pred. No. 0.34;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy 1 WINTYTGQSTYADDFK 16
Db 52 WINTHGVCPKXAEFFK 67
RESULT 9
CR3 SCHPO STANDARD; PRT; 446 AA.
ID CR3 SCHPO STANDARD; PRT; 446 AA.
AC 010272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE WD-repeat protein crb3.
DE Name=crb3; ORFNames=SPAC13G7.08c;
GN Schizosaccharomyces pombe (Pission yeast).
OS Bkayotia; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070339; PubMed=9407031;
RA Saka Y., Ebashi F., Matsusaka T., Mochida S., Yanagida M.;
RT "Damage and replication checkpoint control in fission yeast is ensured
RT by interactions of Crb2, a protein with BRCT motif, with Cuts and
RT Chk1.";
RL Genes Dev. 11:387-3400(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmons M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Wellner-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Meeser D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt K., Pohl T.M.,
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RA Eger P., Zimmermann W., Medler H., Wandutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revela J.L., Moreno S., Armetrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usero D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: Contains 5 WD repeats.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ib-sib.ch).
CC
DR EMBL; AB008572; BAA23358.1; -.
DR EMBL; Z69729; CAA93596.1; -.
DR PIR; T37659; S67437.
DR GeneDB; SPombe; SPAC13G7.08c; -.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011045; WD40_Like.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
FT REPEAT 74
FT REPEAT 113
FT REPEAT 116
FT REPEAT 155
FT REPEAT 172
FT REPEAT 214
FT REPEAT 216
FT REPEAT 257
FT REPEAT 294
FT REPEAT 333
FT REPEAT 49506
FT SEQUENCE 446 AA; 49506 MW; 4C42680926401A1 CRC64;
SO
Query Match 55.7%; Score 54; DB 1; Length 446;
Best Local Similarity 52.9%; Pred. No. 2.3;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Oy 1 WINTYTGQSTYADDFKE 17
Db 243 WIPLYTGSTYPSNNVKE 259
RESULT 10
O6LZ19 PRELIMINARY; PRT; 745 AA.
ID O6LZ19 PRELIMINARY; PRT; 745 AA.
AC O6LZ19;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.
DE OrderedLocusName=MWP0638.
GN Methanococcus maripaludis.
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=52 / LL;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphimachak C., Soli D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT methanogen Methanococcus maripaludis.";
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RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX957220; CAF30194.1; -.
KW Complete proteome.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 745 AA; 84573 MW; 18D85521SDEEB953 CRC64;

Query Match
Best Local Similarity 54.6%; Score 53; DB 2; Length 745;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADD 14
DB 124 WVNYYGQSTYVID 137

RESULT 11
ID Q8A3F1 PRELIMINARY; PRT; 759 AA.
AC Q8A3F1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BT3003;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=819;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjurstedt M.K., Hamrod J., Deng S., Carmichael L.K.,
RA "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RT Science 299:2074-2076 (2003).
RL EMBL; AE016938; AA078109.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001517; TIR.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 759 AA; 88928 MW; 52D975F32501538E CRC64;

Query Match
Best Local Similarity 52.6%; Score 51; DB 2; Length 759;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFK 16
DB 147 WINTFGRSNELDFQ 162

RESULT 12
ID Q7N848 PRELIMINARY; PRT; 2009 AA.
AC Q7N848;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 3.
DE Similitudes with peptide synthetase like pristinamycin I synthase
GN OrderedLocusNames=plu0899;
OS Photobacterium luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TT01;
RX MEDLINE=22957627; PubMed=14528314;

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RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Bouraux-Bude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudreau S.,
RA Medigue C., Lanos A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photobacterium
RT luminescens.";
RT Nat. Biotechnol. 21:1307-1313(2003).
CC -1- SIMILARITY: belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL; BX571861; CAE13194.1; -.
DR HSSP; P14687; IAMU.
DR Photolact; plu0899; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR00873; AMP_bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR006163; Phosphateth_bind.
DR InterPro; IPR006162; Psantne S.
DR InterPro; IPR000501; AMP_binding; 1.
DR Pfam; PF00501; AMP_binding; 1.
DR Pfam; PF00668; Condensation; 2.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW Complete proteome; Phosphopantetheine.
SQ SEQUENCE 2009 AA; 229657 MW; 82CD8C83D7813AC CRC64;

Query Match
Best Local Similarity 49.5%; Score 48; DB 2; Length 2009;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 WINTYTGSTYADDFKE 17
DB 1043 WINTYTBQPIALDQEE 1059

RESULT 13
ID Q7YTW2 PRELIMINARY; PRT; 367 AA.
AC Q7YTW2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein W08G11.1.
GN ORFNames=W08G11.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RT Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Steward C.A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z92817; CAB07296.1; -.
DR WormBase; WBGene00012346; W08G11.1.

```

DR WormPep; W08G11.1; CE16558.
DR InterPro; IPR004951; DUF268.
DR Pfam; PF03269; DUF268; 1.
KM Hypothetical protein.
SQ SEQUENCE 367 AA; 42172 MW; F171013437F28509 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 367;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYGGSTVADDF 15
DB 330 WIDTYSGDSEAFDF 344

RESULT 14

06N091 PRELIMINARY; PRT; 500 AA.
AC 06N091;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C02220 (Fragment).
GN Name=DKFZp686C02220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambolt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX64625; CAE4579.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PR07654; Cl-sec; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_Like; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41B4 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 500;
Best Local Similarity 43.8%; Pred. No. 38;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 WINTYGGSTVADDF 16
DB 87 WISAVSGQTYAQLQ 102

RESULT 15

08A3Y7 PRELIMINARY; PRT; 573 AA.
AC 08A3Y7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative TonB-dependent receptor.
GN OrderedLocuNames=BT2817;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.

OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RT Chiang H.C., Hooper L.V., Gordon J.I.;
RL "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
DR EMBL; AB016937; AA077923.1; -.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
KM Complete proteome; Receptor.
SQ SEQUENCE 573 AA; 64637 MW; 414CB2DCF2F14847 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 573;
Best Local Similarity 52.9%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 WINTYGGSTVADDF 17
DB 390 WINTYGGYQDLKDDFFE 406

Search completed: April 4, 2005, 15:56:06
Job time : 31.7316 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 11.9808 seconds
(without alignments)
193.690 Million cell updates/sec

Title: US-09-887-853-6_COPY_99_104
Perfect score: 34
Sequence: 1 RFGPAY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 34 | 100.0 | 115 | 3 | AA90823 |
| 2 | 34 | 100.0 | 227 | 2 | AA106784 |
| 3 | 34 | 100.0 | 243 | 2 | AAW02280 |
| 4 | 34 | 100.0 | 243 | 2 | AAW53170 |
| 5 | 34 | 100.0 | 243 | 2 | AAW80424 |
| 6 | 34 | 100.0 | 243 | 7 | ABW00716 |
| 7 | 34 | 100.0 | 246 | 2 | AA39569 |
| 8 | 34 | 100.0 | 267 | 2 | AAU04944 |
| 9 | 34 | 100.0 | 453 | 6 | ABU11979 |
| 10 | 34 | 100.0 | 534 | 2 | AA39571 |
| 11 | 31 | 91.2 | 78 | 7 | ADM26258 |
| 12 | 31 | 91.2 | 272 | 4 | ABG05076 |
| 13 | 31 | 91.2 | 300 | 4 | ABG17548 |
| 14 | 31 | 91.2 | 309 | 4 | ABG14667 |
| 15 | 31 | 91.2 | 350 | 7 | ADP59685 |
| 16 | 31 | 91.2 | 361 | 4 | ABG04015 |
| 17 | 31 | 91.2 | 413 | 4 | ABG21008 |
| 18 | 31 | 91.2 | 433 | 4 | ABG07016 |
| 19 | 31 | 91.2 | 730 | 6 | ABU21384 |
| 20 | 30 | 88.2 | 133 | 5 | AAW48375 |
| 21 | 30 | 88.2 | 218 | 3 | AAW74551 |
| 22 | 30 | 88.2 | 218 | 3 | AAW74550 |
| 23 | 30 | 88.2 | 321 | 6 | ABP77987 |
| 24 | 30 | 88.2 | 344 | 4 | ABG18999 |
| 25 | 30 | 88.2 | 571 | 7 | ABO79803 |

ALIGNMENTS

| | | | | | | |
|----|----|------|-----|---|----------|---------------------|
| 26 | 30 | 88.2 | 738 | 8 | ADN19789 | Adn19789 Bacterial |
| 27 | 30 | 88.2 | 776 | 3 | AA96167 | Aa96167 Schizosac |
| 28 | 30 | 88.2 | 858 | 4 | AAU35301 | Aau35301 Enterococ |
| 29 | 30 | 88.2 | 858 | 6 | ABU29233 | Abu29233 Protein e |
| 30 | 30 | 88.2 | 858 | 7 | ADH87543 | Adh87543 Enterococ |
| 31 | 29 | 85.3 | 58 | 4 | AAU53787 | Aau53787 Propionib |
| 32 | 29 | 85.3 | 58 | 6 | ABW50306 | Abw50306 Propionib |
| 33 | 29 | 85.3 | 83 | 6 | ABP80253 | Abp80253 N. gonorr |
| 34 | 29 | 85.3 | 85 | 6 | ABP80721 | Abp80721 N. gonorr |
| 35 | 29 | 85.3 | 85 | 6 | ABP80255 | Abp80255 N. gonorr |
| 36 | 29 | 85.3 | 89 | 4 | AA663385 | Aa663385 Human bre |
| 37 | 29 | 85.3 | 164 | 3 | AA644167 | Aa644167 Arabidops |
| 38 | 29 | 85.3 | 171 | 3 | AA644167 | Aa644167 Arabidops |
| 39 | 29 | 85.3 | 181 | 6 | ABW67792 | Abw67792 Photorhab |
| 40 | 29 | 85.3 | 198 | 3 | AA644166 | Aa644166 Arabidops |
| 41 | 29 | 85.3 | 206 | 8 | ADN46359 | Adn46359 Thermococ |
| 42 | 29 | 85.3 | 215 | 5 | ABP26721 | Abp26721 Streptoco |
| 43 | 29 | 85.3 | 250 | 6 | ABU22431 | Abu22431 Protein e |
| 44 | 29 | 85.3 | 266 | 4 | ABG16569 | Abg16569 Novel hum |
| 45 | 29 | 85.3 | 275 | 4 | ABB64508 | Abb64508 Drosophila |

RESULT 1
AA90823
ID AA90823 standard; protein; 115 AA.
XX
AC AA90823;
DT 29-AUG-2000 (first entry)
DE 520C9 hybridoma VH domain SEQ ID NO:24.
XX
XX
KW Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW antibody; tumour; human; mucin; cancer; cytotoxic; hybridoma;
KW specific binding assay; affinity purification; drug targeting;
KW toxin targeting; imaging; genetic; therapeutic.
XX
OS Homo sapiens.
XX
PN US6054561-A.
XX
PD 25-APR-2000.
XX
PF 07-JUN-1995; 95US-00483749.
XX
PR 08-FEB-1984; 84US-00577976.
PR 11-JAN-1985; 85US-00690750.
PR 21-MAR-1986; 86US-00842476.
PR 08-MAY-1988; 88US-00190778.
PR 11-AUG-1994; 94US-00288981.
XX
PA (CHIR) CHIRON CORP.
XX
PI Ring DB;
XX
DR WPI: 2000-338508/29.
DR N-PSDB; AAA38907.
XX
XX Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer.
XX
PS Disclosure; Fig 12; 57pp; English.
XX
CC The present invention describes a monoclonal antibody (Mab) (I) that
CC binds to a human breast cancer antigen that is also bound by Mab 454C11
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The

CC present sequence represents a VH domain derived from a 520C9 hybridoma,
 CC which is used in the exemplification of the present invention
 XX
 SQ Sequence 115 AA;

Query Match 100.0%; Score 34; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6
 |||||
 Db 99 RFGPAY 104

RESULT 2

AAV06784
 ID AAV06784 standard; protein; 227 AA.

AC AAV06784;

DT 22-JUN-1999 (first entry)

DE M. grisea PTH3 gene product.

KW Fungal pathogenicity; imidazole glycerol phosphate dehydratase; PTH2;
 KM carnitine acetyl transferase; membrane associated pathogenicity protein;
 KM homeodomain transcription factor; PTH3, PTH11, PTH12.

OS Magnaporthe grisea.

PN MO9913094-A2.

PD 18-MAR-1999.

PF 08-SEP-1998; 98WO-US018730.

PR 10-SEP-1997; 97US-0058460P.

(DUPO) DU PONT DE NEMOURS & CO E. I.

PI Sweigard JA;

XX WPI; 1999-229247/19.

DR N-PSDB; AAX32293, AAX32294.

PT New isolated fungal pathogenicity gene.
 PS Claim 15; Page 43-44; 50pp; English.

XX The invention relates to new isolated fungal pathogenicity genes.
 CC designated PTH2, PTH3, PTH11 and PTH12 that are obtained from Magnaporthe
 CC grisea. These novel genes encode proteins (AAV06783-86) that are highly
 CC homologous to the fungal carnitine acetyl transferase enzyme, fungal
 CC imidazole glycerol phosphate dehydratase enzyme, fungal membrane
 CC associated pathogenicity protein or fungal homeodomain transcription
 CC factor respectively. The novel genes are implicated in fungal
 CC pathogenicity. Inhibition of any of the genes PTH2, PTH3, PTH11 and PTH12
 CC results in the reduction or elimination of the pathogenic phenotype of
 CC the fungus. The isolated genes are useful in the design of screens to
 CC identify inhibitors of the fungal pathogenic gene products. The present
 CC sequence represents the amino acid sequence of the PTH3 gene product
 XX
 SQ Sequence 227 AA;

Query Match 100.0%; Score 34; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6
 |||||
 Db 118 RFGPAY 123

RESULT 3
 AAM02280
 ID AAM02280 standard; protein; 243 AA.

AC AAM02280;

DT 25-MAR-2003 (revised)
 DT 29-OCT-1996 (first entry)

DE 520C9 anti-c-erbB-2 two single chain Fv construct.

KW 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;
 KM construct; polypeptide linker; C-terminal amino acid sequence;
 KM in vivo imaging; drug targeting experiment; homodimer; increased;
 KM binding avidity; tissue retention time.

OS Homo sapiens.

FN Key Location/Qualifiers
 FT Peptide 118..133
 FT /label= linker

PN US5534254-A.

PD 09-JUL-1996.

PF 07-OCT-1993; 93US-00133804.

PR 06-FEB-1992; 92US-00831967.

PA (CHTR) CHIRON CORP.
 PA (CREA-) CREATIVE BIOMOLECULES INC.

PI Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI; 1996-333194/33.

DR N-PSDB; AAT36680.

PT Compsns. contg. antigen-targeting antibody fragment constructs -
 PT comprising dimer of single-chain Fv fragments.

PS Example 1; Col 33-36; 30pp; English.

CC Variable heavy (VH) and variable light (VL) genes were cloned from a
 CC 520C9 hybridoma cDNA library, using probes directed toward the antibody
 CC constant and joining regions. A two single chain Fv (sfv) gene was
 CC constructed by connecting the VH and VL genes with a Ser rich polypeptide
 CC linker. The resulting 520C9 two sfv gene, which encodes the present
 CC sequence, was inserted into an expression vector, transformed into E.
 CC coli, and protein expression induced by the addn. of IPTG to the culture
 CC medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be
 CC used for in vivo imaging, and drug targeting experiments. The 2 sfv
 CC protein prod. is a homodimer, in which both fragments target the same
 CC antigen, therefore giving greater binding avidity and longer tissue
 CC retention times, compared to individual sfv protein prod. fragments.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 243 AA;

Query Match 100.0%; Score 34; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6
 |||||
 Db 99 RFGPAY 104

RESULT 4

AAW53170
 ID AAW53170 standard; protein; 243 AA.

AC AAW53170;

```

XX 16-JUN-1998 (first entry)
DT
XX 520C9 anti-c-erbB-2 sFv' dimeric construct protein sequence.
DE
XX Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erbB-2;
KW tumour; diagnosis; ss.
XX
XX Synthetic.
OS Mus sp.
XX
XX US5753204-A.
PN
XX 19-MAY-1998.
PD
XX 05-JUN-1995; 95US-00461838.
PF
XX 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
XX
XX (CHIR ) CHIRON CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Oppermann H, Ring DB, Huston JS, Houston LL;
PI
XX WPI: 1998-311318/27.
DR N-PSDB; AAV21798.
XX
XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv
PT fragments.
XX
XX Example 1; Col 33-36; 30pp; English.
XX
XX This represents the protein sequence of a 520C9 sFv' (single chain Fv)
CC construct. This was constructed by connecting the Vh and Vl genes with a
CC DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can
CC be used in the methods of invention of imaging a preselected antigen
CC expressed in a mammal. The methods are used in magnetic resonance imaging
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
CC constructs have enhanced properties as in vivo targeting agents in
CC comparison with intact monoclonal antibodies or their Fab fragments. The
CC dimeric constructs permit the in vivo targeting of an epitope on an
CC antigen with greater apparent avidity, including greater tumour
CC specificity, tumour localisation and tumour retention properties than
CC that of the Fab fragment having the same CDRs as the construct
XX
XX Sequence 243 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RFGPAY 6
DB 99 RFGPAY 104

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```

PN US5837846-A.
XX
XX 17-NOV-1998.
PD
XX 05-JUN-1995; 95US-00461386.
PF
XX 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CHIR ) CHIRON CORP.
XX
XX Oppermann H, Houston LL, Huston JS, Ring DB;
PI
XX WPI: 1999-023541/02.
DR N-PSDB; AAV63399.
XX
XX Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.
XX
XX Example 1; Col 35-36; 29pp; English.
XX
XX The present sequence represents an antibody 520C9 sFv. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxins, produgs
CC or 99m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumours (especially of ovary or breast)
XX
XX Sequence 243 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RFGPAY 6
DB 99 RFGPAY 104

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RESULT 5
AAW80424
ID AAW80424 standard; protein; 243 AA.
XX
XX AAW80424;
AC
XX 28-JAN-1999 (first entry)
DT
XX 520C9 sFv sequence.
DE
XX 520C9 sFv; antigen; tumour cell; antibody 520C9; targeted delivery;
KW antigen-expressing cell.
XX
XX Synthetic.
XX

```

```

RESULT 6
ABW00716
ID ABW00716 standard; protein; 243 AA.
XX
XX ABW00716;
AC
XX 15-JAN-2004 (first entry)
DT
XX 520C9 sFv protein.
DE
XX Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
KW sFv.
XX
XX Unidentified.
OS
XX US2002168375-A1.
PN
XX 14-NOV-2002.
PD
XX 21-JUN-2001; 2001US-00887853.
PF
XX 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
PR 05-JUN-1995; 95US-00462641.
PR 26-APR-2000; 2000US-00558741.
XX
XX (CHIR ) CHIRON CORP.
PA
XX Huston JS, Houston LL, Ring DB, Oppermann H;
PI
XX

```

DR WPI: 2003-765156/72.
DR N-PSDB; AAD61485.
XX
PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
PS Example 1; Page 19-20; 30pp; English.
XX
CC The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preslected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibits cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 sfv protein. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 34; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RFGPAY 6
DB 99 RFGPAY 104
XX
RESULT 7
AAR39569
ID AAR39569 standard; protein; 246 AA.
XX
AC AAR39569;
XX
DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
DE Sequence of 520C9 sfv protein.
XX
KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW biosynthetic single polypeptide chain binding site; ss.
XX
OS Synthetic.
XX
PN WO9316185-A2.
PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
XX
PR 06-FEB-1992; 92US-00831967.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU) CETUS ONCOLOGY CORP.
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
DR WPI; 1993-272889/34.
DR N-PSDB; AAQ46084.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
XX
PS Claim 4; Page 60-61; 87pp; English.
XX
CC c-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AAQ46083, AAR39568). A single chain Fv (sfv) is a covalently
CC linked VH-VL heterodimer which is expressed from a gene fusion including
CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such

CC linker sequences are set forth in AA residues 116-135 in AAR39569, which
CC includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084
CC for the 520C9 monoclonal antibody, a single chain polypeptide can be
CC produced having a binding affinity for a c-erbB-2 related antigen. 'X' in
CC AAR39569 refers to the location of a stop codon in AAQ46084. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 246 AA;
XX
Query Match 100.0%; Score 34; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RFGPAY 6
DB 99 RFGPAY 104
XX
RESULT 8
AAU04944
ID AAU04944 standard; protein; 267 AA.
XX
AC AAU04944;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE Humanised anti-p185 single chain antibody, 520C9H.
XX
KW Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
KW cancer; tumour; adenocarcinoma.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 53..57
FT /label= CDR
FT /note= "Complementarity determining region"
FT 72..88
FT /label= CDR
FT /note= "Complementarity determining region"
FT 121..126
FT /label= CDR
FT /note= "Complementarity determining region"
FT 138..152
FT /label= Synthetic peptide linker
FT /note= "links the heavy chain to the light chain"
FT 176..186
FT /label= CDR
FT /note= "Complementarity determining region"
FT 202..208
FT /label= CDR
FT /note= "Complementarity determining region"
FT 241..249
FT /label= CDR
FT /note= "Complementarity determining region"
FT 260..267
FT /label= Glu_Glu_epitope
XX
PN WO200153354-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US001919.
XX
PR 20-JAN-2000; 2000US-0177258P.
XX
PA (CHIR) CHIRON CORP.
PA (HAMT-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PA (HAMT-) HAMILTON REGIONAL CANCER CENT.


```
XX Austin R, Kwok CS, Ring DB;
PI WPI; 2001-451904/48.
XX N-PSDB; AAS09507.
DR
XX Novel immunconjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an interleukin-2
PT polypeptide.
XX
XX Claim 7; Fig 9; 74pp; English.
PS
XX The sequence represents a humanised anti-p185 single chain antibody which
CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion
CC protein. The fusion protein (or immunconjugate) is used to inhibit the
CC growth of tumors or cancers particularly those characterised by
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
CC benign tumors of the breast, renal system, salivary gland,
CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 267 AA;

Query Match          100.0%; Score 34; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 121 RFGPAY 126

RESULT 9
ABU11979
ID ABU11979 standard; protein; 453 AA.
XX
AC ABU11979;
XX
DT 23-OCT-2003 (revised)
DT 13-FEB-2003 (first entry)
XX
XX M. echinospora calicheamicin biosynthesis protein CalQ.
DE
XX Calicheamicin biosynthetic gene cluster; aryltetrasaccharide; aglycone;
KM calicheamicin resistance; nonchromoprotein enediylne; enediylne resistance;
KM bone marrow cell; enzyme.
XX
XX Micromonospora echinospora; spp. calichensis.
OS
XX WO200279465-A2.
FN
XX 10-OCT-2002.
PD
XX
XX 28-NOV-2001; 2001WO-US044285.
PF
XX 28-NOV-2000; 2000US-00724797.
FR
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
PA
XX Thorson J;
XX
XX WPI; 2003-092897/08.
DR N-PSDB; AAS56041.
XX
XX Novel nucleic acid molecule from nonchromoprotein enediylne biosynthetic
PT gene cluster from Micromonospora echinospora useful for conferring
PT calicheamicin resistance on a subject.
XX
XX Claim 25; Page 107-108; 179pp; English.
PS
XX The present invention relates to the isolation of the Micromonospora
CC echinospora spp. calichensis calicheamicin biosynthetic gene cluster
CC encoding proteins and enzymes used in the biosynthetic production of
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CC calicheamicin, including aryltetrasaccharide and aglycone. The gene
CC cluster also includes the gene encoding for the protein that confers
CC calicheamicin resistance. The calicheamicin biosynthetic gene cluster is
CC a nonchromoprotein enediylne biosynthetic gene cluster. Expression vectors
CC containing genes from the biosynthetic gene cluster are also disclosed.
CC The expression vectors are useful for producing calicheamicin
CC biosynthetic proteins. The calicheamicin self-resistance gene provides an
CC approach for gene therapy, for example, by introduction of enediylne
CC resistance genes into bone marrow cells, thus increasing resistance and
CC allowing tolerance to chemotherapeutic doses of calicheamicin. ABU11964-
CC ABU12010 represent proteins and enzymes encoded by genes in the M.
CC echinospora calicheamicin biosynthesis gene cluster. (Updated on 23-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 453 AA;

Query Match          100.0%; Score 34; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 443 RFGPAY 448

RESULT 10
AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
AC AAR39571;
XX
DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
XX Sequence of G-FIT.
DE
XX Tumour antigen; C-erbB-2; G-FIT.
XX
XX Synthetic.
OS
XX WO9316185-A2.
XX
XX 19-AUG-1993.
PD
XX
XX 05-FEB-1993; 93WO-US001055.
PF
XX 06-FEB-1992; 92US-00831967.
FR
XX (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU ) CETUS ONCOLOGY CORP.
XX
XX Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX WPI; 1993-272889/34.
DR N-PSDB; AAO46086.
XX
XX New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
PT
XX Example; Page 65-68; 87pp; English.
XX
XX C-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AAO46083, AAR3568) . (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 534 AA;

Query Match          100.0%; Score 34; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 RRGFAY 6
 |||||
 XX 388 RRGFAY 393

RESULT 11
 ADM26258
 ID ADM26258 standard; protein; 78 AA.

XX ADM26258;

XX 20-MAY-2004 (first entry)

DE Hyperthermophile Methanopyrus kandleri protein #864.

KW hyperthermophile; protein stability enhancement;

KM protein activity enhancement.

OS Methanopyrus kandleri.

XX WO2003076575-A2.

XX 18-SEP-2003.

XX 04-MAR-2003; 2003WO-US006664.

XX 04-MAR-2002; 2002US-0361742P.

XX 14-MAY-2002; 2002US-0380423P.

XX 16-SEP-2002; 2002US-0410974P.

PA (FIDE-) FIDELITY SYSTEMS INC.

PI Slesarev AI, Pavlov A, Pavlova N, Kozayavkin S;

XX WPI; 2003-748363/70.

DR N-PSDB; ADM27081.

PT New isolated nucleic acids encoding any of about 1700 Methanopyrus

PT kandleri proteins, and the encoded proteins, useful as a medicaments or

XX as diagnostic agents.

XX Claim 31; SEQ ID NO 864; 1023bp; English.

CC The invention comprises the amino acid sequence of proteins from the
 CC hyperthermophile Methanopyrus kandleri, the invention also comprises the
 CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri
 CC proteins of the invention are useful for enhancing the stability and/or
 CC activity of other proteins. The Methanopyrus kandleri genome is useful in
 CC a variety of diagnostic and analytical methods. The present amino acid
 CC sequence represents a Methanopyrus kandleri protein of the invention.

XX Sequence 78 AA;

Query Match 91.2%; Score 31; DB 7; Length 78;

Best Local Similarity 83.3%; Pred. No. 80;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
 :|||||
 Db 40 KRGFAY 45

RESULT 12

ABG05076
 ID ABG05076 standard; protein; 272 AA.

XX ABG05076;

XX 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #5067.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS69263.

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 20; SEQ ID NO 35435; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX sequences. (I) is useful as hybridisation probes, polymerase chain

XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX and in recombinant production of (II). The polynucleotides are also used

XX in diagnostics as expressed sequence tags for identifying expressed

XX genes. (I) is useful in gene therapy techniques to restore normal

XX activity of (II) or to treat disease states involving (II). (II) is

XX useful for generating antibodies against it, detecting or quantitating a

XX polypeptide in tissue, as molecular weight markers and as a food

XX supplement. (II) and its binding partners are useful in medical imaging

XX of sites expressing (II). (I) and (II) are useful for treating disorders

XX involving aberrant protein expression or biological activity. The

XX polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

XX patent did not appear in the printed specification, but was obtained in

XX electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 272 AA;

Query Match 91.2%; Score 31; DB 4; Length 272;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
 :|||||
 Db 113 RRGFAY 118

RESULT 13

ABG17548
 ID ABG17548 standard; protein; 300 AA.

XX ABG17548;

XX 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #17539.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

```
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS81735.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 47907; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 300 AA;
OY Query Match 91.2%; Score 31; DB 4; Length 300;
OY Best Local Similarity 83.3%; Pred. No. 2.9e+02;
OY Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 RFGPAY 6
OY |:|||
OY 273 RYGFAY 278
DB 273 RYGFAY 278
RESULT 14
ABG14667
ID ABG14667 standard; protein; 309 AA.
XX AC ABG14667;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #14658.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
```

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XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS78854.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 45026; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 309 AA;
OY Query Match 91.2%; Score 31; DB 4; Length 309;
OY Best Local Similarity 83.3%; Pred. No. 3e+02;
OY Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 RFGPAY 6
OY |:|||
OY 215 RYGFAY 220
DB 215 RYGFAY 220
RESULT 15
ADF59685
ID ADF59685 standard; protein; 350 AA.
XX AC ADF59685;
XX DT 12-FEB-2004 (first entry)
XX DE Human polypeptide sequence SEQ ID NO:2052.
XX KW biological activity; genetic engineering; hybridisation probe; oligomer;
XX KW primer; chromosome mapping; gene mapping; recombinant protein production;
XX KW human.
XX OS Homo sapiens.
```

FN WO2003080795-A2.

XX 02-OCT-2003.

PD 09-AUG-2002; 2002WO-US025485.

XX 09-AUG-2001; 2001US-0311261P.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Yang Y, Wang Z, Wang G, Ma Y.

XX WPI: 2003-876918/81.

DR N-PSDB; ADF59603.

XX New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.

XX Claim 20; SEQ ID NO 2052; 571pp; English.

CC The present sequence represents a polypeptide (II) with biological
CC activity, which is encoded by an isolated polynucleotide sequence (I)
CC from the present invention. Also described: (1) a vector comprising (I);
CC (2) an expression vector comprising (I); (3) a host cell genetically
CC engineered to comprise (I) which is operatively associated with a
CC regulatory sequence that modulates expression of (I) in the host cell;
CC (4) a polypeptide (II) encoded by (I); (5) a composition comprising the
CC polypeptide of (4) and a carrier; (6) an antibody directed against the
CC polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a
CC sample; (8) identifying a compound that binds to the polypeptide of (4);
CC (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA.

XX SQ Sequence 350 AA;

Query Match 91.2%; Score 31; DB 7; Length 350;

Best Local Similarity 83.3%; Pred. No. 3.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6

Db 193 RRGFAY 198

Search completed: April 4, 2005, 15:47:20
Job time : 13.9808 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 8.85623 seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6_COPY_99_104

Perfect score: 34

Sequence: 1 RFGPAY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 34 | 100.0 | 243 | 9 | US-09-887-853-6 |
| 2 | 34 | 100.0 | 243 | 17 | US-10-683-547-6 |
| 3 | 34 | 100.0 | 267 | 9 | US-09-766-543-10 |
| 4 | 34 | 100.0 | 276 | 9 | US-09-766-543-12 |
| 5 | 31 | 91.2 | 99 | 15 | US-10-424-599-183438 |
| 6 | 31 | 91.2 | 122 | 15 | US-10-424-599-170913 |
| 7 | 31 | 91.2 | 541 | 16 | US-10-437-963-106568 |
| 8 | 31 | 91.2 | 1015 | 15 | US-10-156-761-9633 |
| 9 | 31 | 91.2 | 1531 | 15 | US-10-282-122A-49308 |
| 10 | 30 | 88.2 | 92 | 15 | US-10-424-599-204252 |
| 11 | 30 | 88.2 | 738 | 15 | US-09-369-493-2442 |
| 12 | 30 | 88.2 | 858 | 9 | US-09-815-242-10894 |
| 13 | 30 | 88.2 | 858 | 15 | US-10-282-122A-57157 |

| 14 | 29 | 85.3 | 60 | 15 | US-10-424-599-220145 | Sequence 220145, A |
|----|----|------|-----|----|----------------------|--------------------|
| 15 | 29 | 85.3 | 65 | 15 | US-10-424-599-208245 | Sequence 208245, A |
| 16 | 29 | 85.3 | 88 | 15 | US-10-424-599-161896 | Sequence 161896, A |
| 17 | 29 | 85.3 | 148 | 16 | US-10-437-963-132767 | Sequence 132767, A |
| 18 | 29 | 85.3 | 153 | 15 | US-10-424-599-159963 | Sequence 159963, A |
| 19 | 29 | 85.3 | 191 | 16 | US-10-767-701-33660 | Sequence 33660, A |
| 20 | 29 | 85.3 | 205 | 15 | US-10-437-963-183461 | Sequence 183461, A |
| 21 | 29 | 85.3 | 231 | 16 | US-10-435-114-63712 | Sequence 63712, A |
| 22 | 29 | 85.3 | 250 | 15 | US-10-282-122A-50355 | Sequence 50355, A |
| 23 | 29 | 85.3 | 252 | 15 | US-10-425-114-50100 | Sequence 60100, A |
| 24 | 29 | 85.3 | 261 | 15 | US-10-425-114-51324 | Sequence 51324, A |
| 25 | 29 | 85.3 | 288 | 14 | US-09-815-242-11689 | Sequence 11689, A |
| 26 | 29 | 85.3 | 296 | 14 | US-10-002-631C-40 | Sequence 40, App1 |
| 27 | 29 | 85.3 | 340 | 15 | US-10-282-122A-53310 | Sequence 53310, A |
| 28 | 29 | 85.3 | 342 | 15 | US-10-282-122A-68785 | Sequence 68785, A |
| 29 | 29 | 85.3 | 343 | 15 | US-10-425-114-44952 | Sequence 44952, A |
| 30 | 29 | 85.3 | 433 | 16 | US-10-437-963-125372 | Sequence 125372, A |
| 31 | 29 | 85.3 | 462 | 15 | US-10-282-122A-51118 | Sequence 51118, A |
| 32 | 29 | 85.3 | 495 | 15 | US-10-369-493-12829 | Sequence 12829, A |
| 33 | 29 | 85.3 | 503 | 16 | US-10-767-701-44045 | Sequence 44045, A |
| 34 | 29 | 85.3 | 541 | 9 | US-09-731-872-278 | Sequence 278, App |
| 35 | 29 | 85.3 | 541 | 9 | US-09-731-872-282 | Sequence 282, App |
| 36 | 29 | 85.3 | 541 | 9 | US-09-731-872-300 | Sequence 300, App |
| 37 | 29 | 85.3 | 541 | 10 | US-09-876-997-278 | Sequence 278, App |
| 38 | 29 | 85.3 | 541 | 10 | US-09-876-997-282 | Sequence 282, App |
| 39 | 29 | 85.3 | 541 | 10 | US-09-876-997-300 | Sequence 300, App |
| 40 | 29 | 85.3 | 541 | 15 | US-10-291-285-238 | Sequence 238, App |
| 41 | 29 | 85.3 | 549 | 15 | US-10-369-493-3466 | Sequence 3466, App |
| 42 | 29 | 85.3 | 558 | 15 | US-10-275-026A-112 | Sequence 112, App |
| 43 | 29 | 85.3 | 564 | 14 | US-10-156-761-6951 | Sequence 6951, App |
| 44 | 29 | 85.3 | 603 | 16 | US-10-437-963-125750 | Sequence 125750, A |
| 45 | 29 | 85.3 | 637 | 15 | US-10-369-493-21603 | Sequence 21603, A |

ALIGNMENTS

RESULT 1
US-09-887-853-6
Sequence 6, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
Oppermann, Hermann
Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Testa, Hurwitz & Thibault/Patent Department
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887, 853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133, 804
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 100.0%; Score 34; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 99 RFGPAY 104

RESULT 2
US-10-683-547-6
Sequence 6, Application US/10683547
Publication No. US20050058638A1
GENERAL INFORMATION:
APPLICANT: Houston, J.
APPLICANT: Houston, J.L.
APPLICANT: Ring, D.
APPLICANT: Oppermann, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: C1BT-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIORITY APPLICATION NUMBER: US/09/558,741
PRIORITY FILING DATE: 2000-04-26
PRIORITY APPLICATION NUMBER: 07/831,967
PRIORITY FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 520C9 sfv
US-10-683-547-6

Query Match 100.0%; Score 34; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 99 RFGPAY 104

RESULT 3
US-09-766-543-10
Sequence 10, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: PP01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIORITY APPLICATION NUMBER: 60/177,258
PRIORITY FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10

LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 520C9
OTHER INFORMATION: humanized single-chain antibody used in the
OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 100.0%; Score 34; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 121 RFGPAY 126

RESULT 4
US-09-766-543-12
Sequence 12, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: PP01679.002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIORITY APPLICATION NUMBER: 60/177,258
PRIORITY FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
OTHER INFORMATION: linker
US-09-766-543-12

Query Match 100.0%; Score 34; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFGPAY 6
DB 121 RFGPAY 126

RESULT 5
US-10-424-599-183438
Sequence 183438, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovacic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 183438
LENGTH: 99
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_136658C.1.pcp

US-10-424-599-183438

Query Match 91.2%; Score 31; DB 15; Length 99;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
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Db 26 KRGPAY 31

RESULT 6

US-10-424-599-170913
; Sequence 170913, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170913
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125349C.1.Dep
US-10-424-599-170913

Query Match 91.2%; Score 31; DB 15; Length 122;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
:|||||
Db 82 KRGPAY 87

RESULT 7

US-10-437-963-106568
; Sequence 106568, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106568
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(541)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_109C.1.Dep
US-10-437-963-106568

Query Match 91.2%; Score 31; DB 16; Length 541;
Best Local Similarity 83.3%; Pred. No. 41e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
:|||||
Db 323 RGFSSY 328

RESULT 8

US-10-156-761-9633
; Sequence 9633, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9633
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9633

Query Match 91.2%; Score 31; DB 14; Length 1015;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
:|||||
Db 541 RTGPAY 546

RESULT 9

US-10-282-122A-49308
; Sequence 49308, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49308
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (611)..(611)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (612)..(612)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (613)..(613)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (614)..(614)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (615)..(615)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (616)..(616)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (617)..(617)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-49308

Query Match          91.2%; Score 31; DB 15; Length 1531;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      888 RYGFAY 893

RESULT 10
US-10-424-599-204252
; Sequence 204252, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204252
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_26467C.1.pep
US-10-424-599-204252

Query Match          88.2%; Score 30; DB 15; Length 92;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      73 RYGFAY 78

RESULT 11
US-10-369-493-2442
; Sequence 2442, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2442
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(738)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2442

Query Match          88.2%; Score 30; DB 15; Length 738;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RFGFAY 6
Db      148 RYGFAY 153

RESULT 12
US-09-815-242-10894
; Sequence 10894, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
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/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10894
/ LENGTH: 858
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
/ US-09-815-242-10894

Query Match      88.2%  Score 30;  DB 9;  Length 858;
Best Local Similarity 83.3%  Pred. No. 1e+03;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 RRGFFAY 6
Db      139 QRGFFAY 144

RESULT 13
/ Sequence 57157, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangou
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zykkind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA, 034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
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/ Remaining Prior Application data removed - See File Wrapper or PATM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 57157
/ LENGTH: 858
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
/ US-10-282-122A-57157

Query Match      88.2%  Score 30;  DB 15;  Length 858;
Best Local Similarity 83.3%  Pred. No. 1e+03;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 RRGFFAY 6
Db      139 QRGFFAY 144

RESULT 14
/ Sequence 220145, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Kovalic, David K
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 220145
/ LENGTH: 60
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_4081C.1.pep
/ US-10-424-599-220145

Query Match      85.3%  Score 29;  DB 15;  Length 60;
Best Local Similarity 83.3%  Pred. No. 1.2e+02;
Matches 5;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1 RRGFFAY 6
Db      31 RRGFFAY 36

RESULT 15
/ Sequence 208245, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J
/ APPLICANT: Kovalic, David K
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 208245
/ LENGTH: 65
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_30070C.1.pep
/ US-10-424-599-208245
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Query Match 85.3%; Score 29; DB 15; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGFAY 6
|||||
Db 41 FGFAY 45

Search completed: April 4, 2005, 16:42:46
Job time : 9.85623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 2.16613 seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6_COPY_99_104

Perfect score: 34

Sequence: 1 RRGFAY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 31 | 91.2 | 208 | 1 | S26196 |
| 3 | 31 | 91.2 | 1008 | 2 | G82732 |
| 4 | 30 | 88.2 | 177 | 2 | T42289 |
| 5 | 30 | 88.2 | 213 | 2 | S73011 |
| 6 | 30 | 88.2 | 336 | 2 | G87202 |
| 7 | 30 | 88.2 | 356 | 2 | C70025 |
| 8 | 30 | 88.2 | 468 | 2 | D83625 |
| 9 | 30 | 88.2 | 776 | 2 | S45495 |
| 10 | 29 | 85.3 | 98 | 2 | F90362 |
| 11 | 29 | 85.3 | 98 | 2 | B99358 |
| 12 | 29 | 85.3 | 137 | 2 | S42467 |
| 13 | 29 | 85.3 | 164 | 2 | G81321 |
| 14 | 29 | 85.3 | 174 | 2 | G64413 |
| 15 | 29 | 85.3 | 213 | 2 | E90356 |
| 16 | 29 | 85.3 | 273 | 2 | D96920 |
| 17 | 29 | 85.3 | 283 | 2 | E90524 |
| 18 | 29 | 85.3 | 299 | 2 | T47003 |
| 19 | 29 | 85.3 | 299 | 2 | AF0238 |
| 20 | 29 | 85.3 | 330 | 2 | F69471 |
| 21 | 29 | 85.3 | 336 | 2 | S74424 |
| 22 | 29 | 85.3 | 387 | 2 | D84700 |
| 23 | 29 | 85.3 | 387 | 2 | D84424 |
| 24 | 29 | 85.3 | 404 | 2 | S27339 |
| 25 | 29 | 85.3 | 558 | 2 | E81037 |
| 26 | 29 | 85.3 | 558 | 2 | E81981 |
| 27 | 29 | 85.3 | 599 | 2 | S15789 |
| 28 | 29 | 85.3 | 637 | 2 | D75123 |
| 29 | 29 | 85.3 | 669 | 2 | T28028 |

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| 30 | 29 | 85.3 | 676 | 2 | F69394 | H+-transporting AT |
| 31 | 29 | 85.3 | 696 | 2 | G88851 | protein Zfx29.10 (|
| 32 | 29 | 85.3 | 760 | 2 | T01441 | hypothetical prote |
| 33 | 29 | 85.3 | 778 | 2 | H96649 | protein F2401.4 [1 |
| 34 | 29 | 85.3 | 843 | 2 | T34618 | NADH2 dehydrogenas |
| 35 | 29 | 85.3 | 998 | 1 | Q08BB1 | B1 protein - black |
| 36 | 29 | 85.3 | 998 | 2 | S41397 | protein A - flock |
| 37 | 28 | 82.4 | 126 | 2 | G83571 | conserved hypothet |
| 38 | 28 | 82.4 | 172 | 2 | A27220 | trypsin inhibitor |
| 39 | 28 | 82.4 | 172 | 2 | A24082 | trypsin inhibitor |
| 40 | 28 | 82.4 | 172 | 2 | JH0780 | trypsin inhibitor |
| 41 | 28 | 82.4 | 205 | 2 | E70199 | competence protein |
| 42 | 28 | 82.4 | 237 | 2 | T16471 | hypothetical prote |
| 43 | 28 | 82.4 | 295 | 2 | E72462 | probable lipolic ac |
| 44 | 28 | 82.4 | 339 | 2 | A97699 | sqdx protein (U453 |
| 45 | 28 | 82.4 | 365 | 2 | AF2893 | glycosyltransferase |

ALIGNMENTS

```
RESULT 1
AC0228      hypothetical protein YP01870 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #ext_change 09-Jul-2004
C/Accession: AC0228
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M., W.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, E
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11585360
A/Accession: AC0228
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-48 <NR>
A/Cross-references: UNIPROT:Q8ZF48; GB:AL590842; PIDN:CA090687.1; PID:G15979892; GSPDB:G
C/Genetics:
A/Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 48;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 RRGFAY 6
Db      30 RRGFAY 35

RESULT 2
S26196      imidazoglycerol-phosphate dehydratase (EC 4.2.1.19) - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
C/Accession: S26196; S19787
R:Goldman, G.H.; Demolder, J.; Dewaele, S.; Herrera-Betrelia, A.; Garemia, R.A.; van Mont
Mol. Gen. Genet. 234, 481-488, 1992
A/Title: Molecular cloning of the imidazoglycerol-phosphate dehydratase gene of Trichode
A/Reference number: S26196; MUID:93024323; PMID:1406594
A/Accession: S26196
A/Molecule type: mRNA
A/Residues: 1-208 <GOL>
A/Cross-references: UNIPROT:P34041; EMBL:Z11528; NID:G5176; PIDN:CA077617.1; PID:G5177
C/Genetics:
A/Query Match
Best Local Similarity 91.2%; Score 31; DB 1; Length 208;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 RRGFAY 6
|||||
Db 120 RRGFAY 125

RESULT 3

hypothetical protein XFI036 [imported] - *Xylella fastidiosa* (strain 9a5c)
C/Species: *Xylella fastidiosa*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: G82732
R/Anonymous: The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: G82732
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1008 <SIM>
A/Cross-references: UNIPROT:Q9PEJ2; GB:AE003940; GB:AE003849; MID:G9105966; PIDN:AAF8384
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, L.E.A.; Carraro, D.M.; Carver, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Senteilly, R.V.; Sawaak M.; Tshakko, M.H.; Vallada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XFI036

Query Match 91.2%; Score 31; DB 2; Length 1008;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
|||||
Db 636 RRGFAY 641

RESULT 4

T42289
hypothetical protein - phage SPPI
C/Species: phage SPPI
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42289
R/Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A/Title: The complete nucleotide sequence and functional organization of *Bacillus subtilis* A/Reference number: Z22137; MUID:98094274; PMID:9334185
A/Accession: T42289
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-177 <ALDO>
A/Cross-references: UNIPROT:O48449; EMBL:X97918; PIDN:CAA6550.1

Query Match 88.2%; Score 30; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
|||||
Db 107 RRGFAY 112

RESULT 5

S73011
hypothetical protein L518_C3_195 - *Mycobacterium leprae*
C/Species: *Mycobacterium leprae*
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S73011
R/Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A/Description: *Mycobacterium leprae* cosmid L518.
A/Reference number: S72591
A/Accession: S73011
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-213 <SM1>
A/Cross-references: UNIPROT:Q49930; EMBL:U00023; MID:g4672194; PIDN:AAA17354.1; PID:g46721
C/Genetics:
A/Start codon: GTG
C/superfamily: *Mycobacterium leprae* hypothetical protein L518_C3_195

Query Match 88.2%; Score 30; DB 2; Length 213;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
|||||
Db 42 RRGFAY 47

RESULT 6

G87202
probable membrane protein [imported] - *Mycobacterium leprae*
C/Species: *Mycobacterium leprae*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87202
R/Cole, S.T.; Biggelaar, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holt R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: G87202
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-336 <STO>
A/Cross-references: UNIPROT:O69510; GB:AL450380; MID:g13093956; PIDN:CAC31863.1; GSPDB:CR A/Genetics:
A/Gene: ML2347

Query Match 88.2%; Score 30; DB 2; Length 336;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGFAY 6
|||||
Db 42 RRGFAY 47

RESULT 7

C70025
multidrug-efflux transporter homolog yuxJ - *Bacillus subtilis*
N/Alternate names: mayB homolog, pbpd 5'-region
C/Species: *Bacillus subtilis*
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: C70025; C55220
R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berier A.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Ertian, K.D.; Errington, J.; Fabrec, C.; Ferratti, E. Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huijlo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rytola, C.; Rocha, A.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Teperstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C70025
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-356 <KUN>
A:Cross-references: UNIPROT:P40760; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15137.
A:Experimental source: strain 168
R:Popham, D.L.; Setlow, P.
J: Bacteriol. 176, 7197-7205, 1994
A:Title: Cloning, nucleotide sequence, mutagenesis, and mapping of the *Bacillus subtilis*
A:Reference number: A55220; MUID:95050302; PMID:7961491
A:Accession: C55220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 101-356 <POP>
A:Cross-references: GB:U11882; NID:9520534; PIDN:AAA64942.1; PID:9520535
C:Genetics:
A:Gene: yuxJ
C:Superfamily: Escherichia coli probable integral membrane protein
Query Match 88.2%; Score 30; DB 2; Length 356;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRGFAY 6
DB 114 RRGFTY 119

RESULT 8
D83625
Probable transporter PA0166 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83625
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim,
. ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83625
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-468 <STO>
A:Cross-references: UNIPROT:Q916W6; GB:AE004454; GB:AE004091; NID:g9945990; PIDN:AA0355
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0166

Query Match 88.2%; Score 30; DB 2; Length 468;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRGFAY 6
DB 245 RRGFAF 250

RESULT 9
S845495
Isop4 protein - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 10-Dec-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S845495, S83741

R:Sato, S.; Suzuki, H.; Widyastuti, U.; Hotta, Y.; Tabata, S.
Curr. Genet. 26, 31-37, 1994
A:Title: Identification and characterization of genes induced during sexual differentiation
A:Reference number: S845492; MUID:95042833; PMID:7954893
A:Accession: S845495
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-776 <SAT>
A:Cross-references: UNIPROT:P40900; EMBL:D14061; NID:g218542; PIDN:BAA03147.1; PID:g21854
C:Genetics:
A:Gene: isp4
C:Superfamily: *Saccharomyces cerevisiae* probable membrane protein YJL212c
Query Match 88.2%; Score 30; DB 2; Length 776;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRGFAY 6
DB 195 RRGFGY 200

RESULT 10
F90362
Hypothetical protein SSO9368 [imported] - *Sulfolobus solfataricus* transposon ISCT1913
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: F90362
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: F90362
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KUR>
A:Cross-references: UNIPROT:Q97WZ4; GB:AE006641; NID:g13815241; PIDN:AAK42157.1; GSPDB:GT
C:Genetics:
A:Gene: SSO9368

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRGFAY 6
DB 20 RRGFEY 25

RESULT 11
B99358
Hypothetical protein SSO9270 [imported] - *Sulfolobus solfataricus* transposon ISCT1913
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B99358
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: B99358
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KUR>
A:Cross-references: UNIPROT:Q97XZ7; GB:AE006641; NID:g13815199; PIDN:AAK42121.1; GSPDB:GT
C:Genetics:
A:Gene: SSO9270

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6
|||||

Db 20 RFGPEX 25

RESULT 12

S42467

Ig heavy chain V region precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S42467

R:Shiyanov, P.A.; Bessalov, I.A.; Tenletskaya, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42466

A:Accession: S42467

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137 <SH1>

A:Cross-references: EMBL:X78107; NID:g460798; PIDN:CAA54997.1; PID:g460799

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFGPAY 6
|||||

Db 122 RFGPAY 126

RESULT 13

G81321

probable integral membrane protein Cj1165c [imported] - Campylobacter jejuni (strain NCT

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: G81321

R:Parhill, J.; Wren, B.W.; Mungall, K.; Kaeley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; WUID:20150912; PMID:10688204

A:Accession: G81321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-164 <PAR>

A:Cross-references: UNIPROT:Q9PND0; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB7341

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1165c

C:Superfamily: primosomal operon 14K protein

Query Match 85.3%; Score 29; DB 2; Length 164;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFGPAY 6
|||||

Db 17 RFGPAY 21

RESULT 14

F64413

hypothetical protein M70910 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: F64413

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

J. Reich, C.I.; Overbeek, R.; Kirnesh, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex, A.;

reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; WUID:96337999; PMID:8688087

A:Accession: F64413

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-174 <BU1>

A:Cross-references: UNIPROT:Q58320; GB:U67534; GB:L77117; NID:g1591579; PIDN:AA898912.1;

C:Genetics:

A:Map position: REV841956-841432

Query Match 85.3%; Score 29; DB 2; Length 174;

Best Local Similarity 83.3%; Pred. No. 57;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6
|||||

Db 147 RFGPKY 152

RESULT 15

E90356

hypothetical protein SSO1915 [imported] - Sulfolobus solfataricus transposon ISCI913

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: E90356

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-Y

Jong, I.; Jeffries, A.C.; Kozera, C.D.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.

arrett, R.A.; Ragan, M.A.; Jensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: E90356

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-213 <KUR>

A:Cross-references: UNIPROT:Q97X40; GB:AE006641; NID:g13815184; PIDN:AAK42108.1; GSPDB:GT

C:Genetics:

A:Gene: SSO1915

Query Match 85.3%; Score 29; DB 2; Length 213;

Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFGPAY 6
|||||

Db 135 RFGPEX 140

Search completed: April 4, 2005, 15:58:05
Job time : 3.16613 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 10.1406 seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6_COPY_99_104
Perfect score: 34
Sequence: 1 RFGPAY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 34 | 100.0 | 178 | 2 | Q9LSY6 wolbachia e |
| 2 | 34 | 100.0 | 185 | 2 | Q931J0 wolbachia s |
| 3 | 34 | 100.0 | 185 | 2 | Q931J2 wolbachia s |
| 4 | 34 | 100.0 | 185 | 2 | Q931J3 wolbachia s |
| 5 | 34 | 100.0 | 185 | 2 | Q9RBD2 wolbachia s |
| 6 | 34 | 100.0 | 185 | 2 | Q9RBD3 wolbachia s |
| 7 | 34 | 100.0 | 185 | 2 | Q9RBD4 wolbachia s |
| 8 | 34 | 100.0 | 185 | 2 | Q9ZM45 wolbachia s |
| 9 | 34 | 100.0 | 185 | 2 | Q9ZM46 wolbachia s |
| 10 | 34 | 100.0 | 186 | 2 | Q9LSY4 wolbachia e |
| 11 | 34 | 100.0 | 186 | 2 | Q9LSY5 wolbachia e |
| 12 | 34 | 100.0 | 186 | 2 | Q9LSY7 wolbachia e |
| 13 | 34 | 100.0 | 186 | 2 | Q9LSY8 wolbachia e |
| 14 | 34 | 100.0 | 186 | 2 | Q9LSY9 wolbachia e |
| 15 | 34 | 100.0 | 190 | 2 | Q6GV15 wolbachia e |
| 16 | 34 | 100.0 | 199 | 2 | Q841P2 wolbachia e |
| 17 | 34 | 100.0 | 227 | 1 | H1S7 MAGGR |
| 18 | 34 | 100.0 | 453 | 2 | Q8KNF6 |
| 19 | 34 | 100.0 | 1043 | 1 | RPRO NODAV |
| 20 | 31 | 91.2 | 48 | 2 | Q6EB95 |
| 21 | 31 | 91.2 | 48 | 2 | Q8ZF48 |
| 22 | 31 | 91.2 | 78 | 2 | Q8TH48 |
| 23 | 31 | 91.2 | 188 | 2 | Q9AMB3 |
| 24 | 31 | 91.2 | 201 | 2 | Q8KO75 |
| 25 | 31 | 91.2 | 201 | 2 | Q8KO76 |
| 26 | 31 | 91.2 | 208 | 1 | H1S7_FRIHA |
| 27 | 31 | 91.2 | 222 | 2 | Q8VU08 |
| 28 | 31 | 91.2 | 303 | 2 | Q8XVMO |
| 29 | 31 | 91.2 | 322 | 2 | Q7R018 |
| 30 | 31 | 91.2 | 408 | 2 | Q7MIS1 |
| 31 | 31 | 91.2 | 408 | 2 | Q8DB51 |

| | | | | | | |
|----|----|------|------|---|--------|---------------------|
| 32 | 31 | 91.2 | 612 | 2 | Q8XTA6 | O8xra6 ralestonia s |
| 33 | 31 | 91.2 | 700 | 2 | Q6C7R4 | Q6c7r4 yarrowia li |
| 34 | 31 | 91.2 | 826 | 2 | Q8EGG7 | Q8egg7 shewanella |
| 35 | 31 | 91.2 | 1008 | 2 | Q87E19 | Q87e19 xylella fas |
| 36 | 31 | 91.2 | 1008 | 2 | Q9PEJ2 | Q9pej2 xylella fas |
| 37 | 31 | 91.2 | 1010 | 2 | Q8P3D9 | Q8p3d9 xanthomonas |
| 38 | 31 | 91.2 | 1011 | 2 | Q8PER6 | Q8per6 xanthomonas |
| 39 | 31 | 91.2 | 1015 | 2 | Q821B5 | Q821b5 streptomyces |
| 40 | 30 | 88.2 | 156 | 2 | Q7OK09 | Q7ok09 bacillus am |
| 41 | 30 | 88.2 | 177 | 2 | Q48449 | Q48449 bacterioph |
| 42 | 30 | 88.2 | 197 | 2 | Q8WY49 | Q8wy49 homo sapien |
| 43 | 30 | 88.2 | 213 | 2 | Q49930 | Q49930 mycobacteri |
| 44 | 30 | 88.2 | 223 | 2 | Q8EC38 | Q8ec38 pseudomonas |
| 45 | 30 | 88.2 | 234 | 2 | Q6FDU4 | Q6fd4 acinetobact |

ALIGNMENTS

| | | | | | | | | | |
|--|---|--------|-----|-------|-----|-----------------|--------|--|--|
| RESULT 1 | | | | | | | | | |
| Q9LSY6 | PRELIMINARY; | PRT; | 178 | AA. | | | | | |
| AC | Q9LSY6; | | | | | | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Created) | | | | | | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | | | | | | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | | | | | | |
| DE | Outer surface protein (Fragment). | | | | | | | | |
| GN | Name=wsp; | | | | | | | | |
| OS | Wolbachia endosymbiont of Trichogramma embryophagum. | | | | | | | | |
| OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; | | | | | | | | |
| OC | Rickettsiaceae; Wolbachiae; Wolbachia. | | | | | | | | |
| OK | NCBI_TaxID=125595; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=Uro3; | | | | | | | | |
| RX | MEDLINE=20496957; PubMed=11040288; | | | | | | | | |
| RA | Pintureau B, Chaudier S, Laasabiere F, Charles H, Grenier S; | | | | | | | | |
| RT | "Addition of wsp sequences to the Wolbachia phylogenetic tree and | | | | | | | | |
| RT | stability of the classification." | | | | | | | | |
| RL | J. Mol. Evol. 51:374-377(2000). | | | | | | | | |
| DR | EMBL; AF245165; AAF71319.1; " | | | | | | | | |
| DR | InterPro; IPR002566; Surface_Ag_msp4. | | | | | | | | |
| DR | Pfam; PF01617; Surface_Ag_2; 2. | | | | | | | | |
| FT | NON_TER | 1 | | | | | | | |
| FT | NON_TER | 178 | | | | | | | |
| FT | SEQUENCE | 178 | AA; | 19235 | MM; | BF6BA9735106689 | CRC64; | | |
| Query Match | | | | | | | | | |
| Beer Local Similarity 100.0%; Score 34; DB 2; Length 178; | | | | | | | | | |
| Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | RFGPAY | 6 | | | | | | |
| DB | 129 | RFGPAY | 134 | | | | | | |
| RESULT 2 | | | | | | | | | |
| Q931J0 | PRELIMINARY; | PRT; | 185 | AA. | | | | | |
| AC | Q931J0; | | | | | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | | | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | | | | | | |
| DT | 01-JUN-2003 (TREMBLrel. 24, Last annotation update) | | | | | | | | |
| DE | Outer surface protein (Fragment). | | | | | | | | |
| GN | Name=wsp; | | | | | | | | |
| OS | Wolbachia sp. wBraf6. | | | | | | | | |
| OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; | | | | | | | | |
| OC | Rickettsiaceae; Wolbachiae; Wolbachia. | | | | | | | | |
| OK | NCBI_TaxID=133462; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=wBraf6; | | | | | | | | |
| RX | MEDLINE=22867875; PubMed=14506854; | | | | | | | | |

```
RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291377; CAC44877.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
DR NON_TER 1 185  
FT NON_TER 185  
SQ SEQUENCE 185 AA; 19843 MW; F2209E49DF904F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

```
RESULT 3  
Q93IJ2 PRELIMINARY; PRT; 185 AA.  
ID Q93IJ2  
AC Q93IJ2; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wBtab4.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=133460;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wBtab4;  
RX MEDLINE=22867875; PubMed=14506854;  
RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291375; CAC44875.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
DR NON_TER 1 185  
FT NON_TER 185  
SQ SEQUENCE 185 AA; 19809 MW; F2209E49D3634F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

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RX MEDLINE=22867875; PubMed=14506854;  
RA Niranjanaki A., Banks G.K., Frohlich D., Veneti D.R., Braig H.R.,  
RA Miller T.A., Bedford I.D., arkham P.G., Savakis C., Bourtzis K.,  
RT "Wolbachia infections of the whitefly Bemisia tabaci."  
RL Curr. Microbiol. 47:93-101(2003).  
DR EMBL; AJ291374; CAC44874.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
DR NON_TER 1 185  
FT NON_TER 185  
SQ SEQUENCE 185 AA; 19809 MW; F2209E49D3634F58 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

```
RESULT 5  
Q9R8D2 PRELIMINARY; PRT; 185 AA.  
ID Q9R8D2  
AC Q9R8D2; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wBtab.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=77832;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wBtab;  
RX MEDLINE=99398205; PubMed=10469257;  
RA van Meer M.M.M., Witteveldt V., Scouthamer R.,  
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp  
gene."  
RL Insect Mol. Biol. 8:399-408(1999).  
DR EMBL; AF071928; AAC77406.1; "-"  
DR InterPro; IPR002566; Surface_Ag_msp4.  
DR Pfam; PF01617; Surface_Ag_2; 2.  
DR NON_TER 1 185  
FT NON_TER 185  
SQ SEQUENCE 185 AA; 20030 MW; 48424234CCE60431 CRC64;  
  
Query Match 100.0%; Score 34; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFGPAY 6  
Db 128 RFGPAY 133
```

```
RESULT 4  
Q93IJ3 PRELIMINARY; PRT; 185 AA.  
ID Q93IJ3  
AC Q93IJ3; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wBtab3.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=133459;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wBtab3;
```

```
RESULT 6  
Q9R8D3 PRELIMINARY; PRT; 185 AA.  
ID Q9R8D3  
AC Q9R8D3; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Outer surface protein (Fragment).  
GN Name=msp;  
OS Wolbachia sp. wBtab.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Wolbachiae; Wolbachia.  
OX NCBI_TaxID=77831;  
RN [1]  
RP SEQUENCE FROM N.A.
```


RC STRAIN=WD61SM;
RA MEDLINE=99398205; PubMed=10469257;
RX van Meer M.M.M., Witteveldt J., Scoutthamer R.;
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp
gene."
RT Insect Mol. Biol. 8:399-408(1999).
DR EMBL, AF071925; AAC77405.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 20045 MW; 52F2439260ED0E91 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
Db 128 RFGPAY 133

RESULT 7

Q9ZH44 PRELIMINARY; PRT; 185 AA.
ID Q9ZH44
AC Q9ZH44;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=WSP;
OS Wolbachia sp. wKayLC.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=77833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wKayLC;
RX MEDLINE=99398205; PubMed=10469257;
RA van Meer M.M.M., Witteveldt J., Scoutthamer R.;
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp
gene."
RT Insect Mol. Biol. 8:399-408(1999).
RL EMBL, AF071927; AAC77407.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 19990 MW; 1F1D66A2B72F4E62 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
Db 128 RFGPAY 133

RESULT 8

Q9ZH45 PRELIMINARY; PRT; 185 AA.
ID Q9ZH45
AC Q9ZH45;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=WSP;
OS Wolbachia sp. wKayB.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=77830;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=wKayB.
RX MEDLINE=99398205; PubMed=10469257;
RA van Meer M.M.M., Witteveldt J., Scoutthamer R.;
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp
gene."
RT Insect Mol. Biol. 8:399-408(1999).
DR EMBL, AF071924; AAC77404.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 20044 MW; 52F2439FDEDD0E91 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
Db 128 RFGPAY 133

RESULT 9

Q9ZH46 PRELIMINARY; PRT; 185 AA.
ID Q9ZH46
AC Q9ZH46;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=WSP;
OS Wolbachia sp. wSib.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=77829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wSib;
RX MEDLINE=99398205; PubMed=10469257;
RA van Meer M.M.M., Witteveldt J., Scoutthamer R.;
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp
gene."
RT Insect Mol. Biol. 8:399-408(1999).
RL EMBL, AF071923; AAC77403.1; -
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 19997 MW; 93E9C36F2B8F6F19 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFGPAY 6
Db 128 RFGPAY 133

RESULT 10

Q9LSY4 PRELIMINARY; PRT; 186 AA.
ID Q9LSY4
AC Q9LSY4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma evanescens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=125597;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M36;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245167; AAF71321.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20088 MW; 911EAFABDF6451DF CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 11
Q9L5Y5 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma oleae.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=125596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M36;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245167; AAF71320.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20144 MW; 230A17BA67089A91 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 12
Q9L5Y7 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma cordubensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
```

```
OX NCBI_TaxID=125594;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Grey;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245164; AAF71318.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20088 MW; 911EAFABDF6451DF CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 13
Q9L5Y8 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma pretiosum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=125593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T191;
RX MEDLINE=20496957; PubMed=11040288;
RA Pintureau B., Chaudier S., Lassabliere F., Charles H., Grenier S.;
RT "Addition of wsp sequences to the Wolbachia phylogenetic tree and
RL stability of the classification.";
RL J. Mol. Evol. 51:374-377(2000).
DR EMBL; AF245163; AAF71317.1; -.
DR InterPro; IPR002566; Surface_Ag_msp4.
DR Pfam; PF01617; Surface_Ag_2; 2.
FT NON_TER
FT NON_TER
SQ SEQUENCE 186 AA; 20144 MW; 230A17BA67089A91 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 2; Length 186;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGFAY 6
DB 129 RRGFAY 134

RESULT 14
Q9L5Y9 PRELIMINARY; PRT; 186 AA.
AC Q9L5Y9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Outer surface protein (Fragment).
GN Name=wsp;
OS Wolbachia endosymbiont of Trichogramma semblidis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
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OC Rickettsiaceae; Wolbachiae; Wolbachia.
 OX NCBI_TaxId=125592;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=semv;
 RX MEDLINE=20496957; PubMed=11040288;
 RA Pintureau B., Chaudier S., Laesabliere F., Charles H., Grenier S.;
 RT "Addition of wap sequences to the Wolbachia phylogenetic tree and
 RL stability of the classification."; J. Mol. Evol. 51:374-377(2000).
 DR EMBL; AF245162; AAF71316.1; -;
 DR InterPro; IPR002566; Surface_Ag_msp4.
 DR Pfam; PF01617; Surface_Ag_2; 2.
 FT NON_TER 1 186
 SQ SEQUENCE 186 AA; 20158 MW; 56013C0E2C07DFC8 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6
 DB 129 RFGPAY 134

RESULT 15

OGGV15 PRELIMINARY; PRT; 190 AA.
 AC OGGV15;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Outer surface protein (Fragment).
 GN Name=wap;
 OS Wolbachia endosymbiont of Trichogramma dendrolimi.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Wolbachiae; Wolbachia.
 OX NCBI_TaxId=164403;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang C.M., Cong B., Dai Q.H., Fu H.B.;
 RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY634680; AAT48492.1; -;
 DR InterPro; IPR002566; Surface_Ag_msp4.
 DR Pfam; PF01617; Surface_Ag_2; 1.
 FT NON_TER 1 190
 SQ SEQUENCE 190 AA; 20614 MW; 1861F43336D01621 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFGPAY 6
 DB 127 RFGPAY 132

Search completed: April 4, 2005, 15:56:21
 Job time : 12.1406 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 485.224 Seconds
(without alignments)
193.690 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EIQLVQSGPELKKRGFTYKI.....YAIPFYTGSGTNLE...KRAD 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: _geneseqp19808:*\n2: _geneseqp19908:*\n3: _geneseqp20008:*\n4: _geneseqp20018:*\n5: _geneseqp20028:*\n6: _geneseqp20038:*\n7: _geneseqp20038:*\n8: _geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1258 | 100.0 | 243 | 2 | AAW02280 520C9 ant |
| 2 | 1258 | 100.0 | 243 | 2 | AAW53170 520C9 ant |
| 3 | 1258 | 100.0 | 243 | 2 | AAW80424 520C9 sFv |
| 4 | 1258 | 100.0 | 243 | 7 | ABW00716 520C9 sFv |
| 5 | 1258 | 100.0 | 246 | 2 | AAW39569 Sequence |
| 6 | 1206 | 95.9 | 534 | 2 | AAW39571 Sequence |
| 7 | 1055 | 83.9 | 409 | 4 | AAU04845 Humanised |
| 8 | 976 | 77.6 | 499 | 5 | AAU72872 Humanised |
| 9 | 950.5 | 75.6 | 267 | 4 | AAU04944 Humanised |
| 10 | 914 | 72.7 | 250 | 2 | AAW02278 741F8 ant |
| 11 | 914 | 72.7 | 250 | 2 | AAW02261 741F8 ant |
| 12 | 914 | 72.7 | 250 | 2 | AAW47012 Single ch |
| 13 | 914 | 72.7 | 250 | 2 | AAW47012 Single ch |
| 14 | 914 | 72.7 | 250 | 2 | AAW53168 741F8 ant |
| 15 | 914 | 72.7 | 250 | 2 | AAW80422 741F8 ant |
| 16 | 914 | 72.7 | 250 | 7 | ABW00714 741F8 sFv |
| 17 | 879 | 68.9 | 667 | 2 | AAW39573 Sequence |
| 18 | 857.5 | 68.2 | 237 | 3 | AAW44595 sFv#125 |
| 19 | 857.5 | 68.2 | 243 | 3 | AAW44596 sFv#125 |
| 20 | 857 | 68.1 | 259 | 7 | ADG32322 Mouse sCF |
| 21 | 857 | 68.1 | 329 | 7 | ADG32325 Precursor |
| 22 | 842 | 66.9 | 259 | 7 | ADG32324 Mouse sCF |
| 23 | 842 | 66.9 | 329 | 7 | ADG32321 Precursor |
| 24 | 841.5 | 66.9 | 240 | 8 | ADN16154 Mouse C7 |
| 25 | 840.5 | 66.8 | 242 | 4 | AAW20433 Anti-FIX/ |

| | | | | | |
|----|-------|------|------|---|---------------------|
| 26 | 830.5 | 66.0 | 461 | 2 | AAW85508 Leader-sc |
| 27 | 823.5 | 65.5 | 530 | 2 | AAW95053 sCFv(FRP5 |
| 28 | 823.5 | 65.5 | 615 | 2 | AAW95056 GAL4-DT-8 |
| 29 | 823.5 | 65.5 | 617 | 2 | AAW95057 GAL4-DT-8 |
| 30 | 823.5 | 65.5 | 651 | 2 | AAW05136 sCFv(FRP5 |
| 31 | 823.5 | 65.5 | 699 | 2 | AAW05138 sCFv(FRP5 |
| 32 | 823.5 | 65.5 | 711 | 2 | AAW26980 Fv(FRP5) - |
| 33 | 823.5 | 65.5 | 892 | 2 | AAW05140 sCFv2 (225 |
| 34 | 823.5 | 65.5 | 892 | 2 | AAW05143 sCFv2 (FRP |
| 35 | 823.5 | 65.5 | 892 | 2 | AAW05139 sCFv2 (FRP |
| 36 | 823.5 | 65.5 | 895 | 2 | AAW05142 sCFv2 (FRP |
| 37 | 823.5 | 65.5 | 899 | 2 | AAW05144 sCFv2 (FRP |
| 38 | 823.5 | 65.5 | 1020 | 2 | AAW05141 sCFv2 (FRP |
| 39 | 820.5 | 65.2 | 637 | 2 | AAW26982 (FRP5) -RT |
| 40 | 818.5 | 65.1 | 240 | 2 | AAW85494 sFvB-2-sFv |
| 41 | 818.5 | 65.1 | 240 | 2 | AAW05134 Single ch |
| 42 | 818 | 65.0 | 252 | 5 | AAU72863 P4-14 sFv |
| 43 | 816 | 64.9 | 259 | 3 | AAW09779 Anti-viral |
| 44 | 815.5 | 64.8 | 251 | 7 | ADG32321 Mouse sCF |
| 45 | 815.5 | 64.8 | 320 | 7 | ADG32358 Precursor |

ALIGNMENTS

| | | | | | |
|----------|---|---------------------|--|--|--|
| RESULT 1 | | | | | |
| AAW02280 | standard; protein; 243 AA. | | | | |
| ID | AAW02280 | | | | |
| XX | | | | | |
| AC | AAW02280; | | | | |
| XX | | | | | |
| DT | 25-MAR-2003 (revised) | | | | |
| DT | 29-OCT-1996 (first entry) | | | | |
| DE | 520C9 anti-c-erbB-2 two single chain Fv construct. | | | | |
| XX | | | | | |
| KW | 520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv; | | | | |
| KW | construct; polypeptide linker; C-terminal; amino acid sequence; | | | | |
| KW | in vivo imaging; drug targeting experiment; homodimer; increased; | | | | |
| KW | binding avidity; tissue retention time. | | | | |
| XX | | | | | |
| OS | Homo sapiens. | | | | |
| XX | | | | | |
| PH | Key | Location/Qualifiers | | | |
| FT | Peptide | 118..133 | | | |
| FT | | /label= linker | | | |
| XX | | | | | |
| PN | US5534254-A. | | | | |
| XX | | | | | |
| PD | 09-JUL-1996. | | | | |
| XX | | | | | |
| PF | 07-OCT-1993; 93US-00133804. | | | | |
| XX | | | | | |
| PR | 06-FEB-1992; 92US-0081967. | | | | |
| XX | | | | | |
| PA | (CHIR) CHIRON CORP. | | | | |
| PA | (CREA-) CREATIVE BIOMOLECULES INC. | | | | |
| PI | Opfermann H, Ring DB, Huston JS, Huston LL; | | | | |
| DR | WPI, 1996-333194/33. | | | | |
| XX | N-PSDB; AAT36880. | | | | |
| PT | Compsns. contg. antigen-targeting antibody fragment constructs - | | | | |
| PT | comprising dimer of single-chain Fv fragments. | | | | |
| XX | | | | | |
| PS | Example 1; Col 33-36; 30pp; English. | | | | |
| XX | | | | | |
| CC | Variable heavy (VH) and variable light (VL) genes were cloned from a | | | | |
| CC | 520C9 hybridoma cDNA library, using probes directed toward the antibody | | | | |
| CC | constant and joining regions. A two single chain Fv (sFv) gene was | | | | |
| CC | constructed by connecting the VH and VL genes with a Ser rich polypeptide | | | | |
| CC | linker. The resulting 520C9 two sFv gene, which encodes the present | | | | |

CC sequence, was inserted into an expression vector, transformed into E.
CC coli, and protein expression induced by the addn. of IPTG to the culture
CC medium. A compsn. comprising a carrier and the 2 sfv protein prod. can be
CC used for in vivo imaging, and drug targeting experiments. The 2 sfv
CC protein prod. is a homodimer, in which both fragments target the same
CC antigen, therefore giving greater binding avidity and longer tissue
CC retention times, compared to individual sfv protein prod. fragments.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC
XX

Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60
DB 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60
QY 61 ADPKERFAFSLKTSATTAAHQLINNLNEDSATYFCARRFGFAVWGQTLVSVASISSS 120
DB 61 ADPKERFAFSLKTSATTAAHQLINNLNEDSATYFCARRFGFAVWGQTLVSVASISSS 120
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
QY 181 IYATSSLDGVPKRPFGSGRSGSDYSLTSSLESDFVYVYCLQYAIPTYPFGGNTLEIK 240
DB 181 IYATSSLDGVPKRPFGSGRSGSDYSLTSSLESDFVYVYCLQYAIPTYPFGGNTLEIK 240
QY 241 RAD 243
DB 241 RAD 243

RESULT 2

AAM53170
ID AAM53170 standard; protein; 243 AA.

XX AAM53170;

DT 16-JUL-1998 (first entry)

DE 520C9 anti-c-erbB-2 sfv' dimeric construct protein sequence.

XX Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;
KM tumour; diagnosis; ss.
XX
OS Synthetic.
OS Mus sp.

PN US5753204-A.

PD 19-MAY-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Ring DB, Huston JS, Houston LL;

DR WPI, 1998-311318/27.

DR N-PSDB; AAV21798.

XX Imaging of antigens in vivo - using dimers of single-chain antibody Fv
PT fragments.
XX

PS Example 1; Col 33-36; 30pp; English.

XX This represents the protein sequence of a 520C9 sfv' (single chain Fv)
CC construct. This was constructed by connecting the Vh and Vl genes with a
CC DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal
CC antibody useful in targeting c-erbB-2 antigen. This dimeric construct can
CC be used in the methods of invention of imaging a preselected antigen
CC expressed in a mammal. The methods are used in magnetic resonance imaging
CC of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic
CC constructs have enhanced properties as in vivo targeting agents in
CC comparison with intact monoclonal antibodies or their Fab fragments. The
CC dimeric constructs permit the in vivo targeting of an epitope on an
CC antigen with greater apparent avidity, including greater tumour
CC specificity, tumour localisation and tumour retention properties than
CC that of the Fab fragment having the same CDRs as the construct
CC
XX

Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60
DB 1 EIQLVQSGPELKKPGETVTKISCKASGYTFPANYGMNMWKAQPGKGLKMWGINTYTGOSTY 60
QY 61 ADPKERFAFSLKTSATTAAHQLINNLNEDSATYFCARRFGFAVWGQTLVSVASISSS 120
DB 61 ADPKERFAFSLKTSATTAAHQLINNLNEDSATYFCARRFGFAVWGQTLVSVASISSS 120
QY 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPPDGTIKRL 180
QY 181 IYATSSLDGVPKRPFGSGRSGSDYSLTSSLESDFVYVYCLQYAIPTYPFGGNTLEIK 240
DB 181 IYATSSLDGVPKRPFGSGRSGSDYSLTSSLESDFVYVYCLQYAIPTYPFGGNTLEIK 240
QY 241 RAD 243
DB 241 RAD 243

RESULT 3

AAM80424
ID AAM80424 standard; protein; 243 AA.

XX AAM80424;

DT 28-JAN-1999 (first entry)

DE 520C9 sfv sequence.

XX 520C9 sfv; antigen; tumour cell; antibody 520C9; targeted delivery;
KM antigen-expressing cell.
XX
OS Synthetic.

PN US5837846-A.

PD 17-NOV-1998.

PF 05-JUN-1995; 95US-00461838.

PR 06-FEB-1992; 92US-00831967.

PR 07-OCT-1993; 93US-00133804.

PA (CHIR) CHIRON CORP.

PA (CREA-) CREATIVE BIOMOLECULES INC.

XX Oppermann H, Houston LL, Huston JS, Ring DB;

DR WPI, 1999-023541/02.

DR N-PSDB; AAV63399.

XX Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumors.

PS Example 1; Col 35-36; 29pp; English.

XX The present sequence represents an antibody 520C9 sFv. Variable heavy and
CC light sequences of antibody 7520C9 are connected, together with a serine
CC linker, to produce the present single chain Fv gene. The present sequence
CC exemplifies the invention. Dimers of the single chain Fv are used for
CC targeted delivery of drugs or imaging agents (e.g. cytotoxic, products
CC or 39m-technetium) to antigen-expressing cells, particularly for
CC treatment or diagnosis of tumors (especially of ovary or breast)

XX Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 8.8e-88;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQIVQSGELKKPGETVKISKASGYTPANYGMNMMKQAPGKGLKMGNTITYGQSTY 60
DB 1 EIQIVQSGELKKPGETVKISKASGYTPANYGMNMMKQAPGKGLKMGNTITYGQSTY 60

QY 61 ADDPKERFAFSLTETSATTAAHLQINLRNEDSATYFCARFPGFAYWQGTLVSVASISSS 120
DB 61 ADDPKERFAFSLTETSATTAAHLQINLRNEDSATYFCARFPGFAYWQGTLVSVASISSS 120

QY 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180

QY 181 IYATSSLDGVPKRFSGSRSGSDYSLTISLSEDFVYVYCCIQYAIFPTFGGNTLEIK 240
DB 181 IYATSSLDGVPKRFSGSRSGSDYSLTISLSEDFVYVYCCIQYAIFPTFGGNTLEIK 240

QY 241 RAD 243
DB 241 RAD 243

RESULT 4

ABM00716 standard; protein; 243 AA.

XX ABM00716;

XX 15-JAN-2004 (first entry)

XX 520C9 sFv protein.

XX Cell proliferation; cytotoxic agent; drug targeting; single-chain Fv;
KW sFv.

XX Unidentified.

XX US2002168375-A1.

XX 14-NOV-2002.

XX 21-JUN-2001; 2001US-00887853.

XX 06-FEB-1992; 92US-00831967.

XX 07-OCT-1993; 93US-00133804.

XX 05-JUN-1995; 95US-00462641.

XX 26-APR-2000; 2000US-00558741.

XX (CHIR) CHIRON CORP.

XX Huston JS, Houston LL, Ring DB, Oppermann H;

DR WPI: 2003-765156/72.

DR N-PSDB; AAD61485.

XX Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.

XX Example 1; Page 19-20; 30pp; English.

XX The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibit cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 520C9 sFv protein. This sequence is used in the exemplification of the
CC invention

XX Sequence 243 AA;

Query Match 100.0%; Score 1258; DB 7; Length 243;

Best Local Similarity 100.0%; Pred. No. 9.8e-88;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQIVQSGELKKPGETVKISKASGYTPANYGMNMMKQAPGKGLKMGNTITYGQSTY 60
DB 1 EIQIVQSGELKKPGETVKISKASGYTPANYGMNMMKQAPGKGLKMGNTITYGQSTY 60

QY 61 ADDPKERFAFSLTETSATTAAHLQINLRNEDSATYFCARFPGFAYWQGTLVSVASISSS 120
DB 61 ADDPKERFAFSLTETSATTAAHLQINLRNEDSATYFCARFPGFAYWQGTLVSVASISSS 120

QY 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 121 SSSSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180

QY 181 IYATSSLDGVPKRFSGSRSGSDYSLTISLSEDFVYVYCCIQYAIFPTFGGNTLEIK 240
DB 181 IYATSSLDGVPKRFSGSRSGSDYSLTISLSEDFVYVYCCIQYAIFPTFGGNTLEIK 240

QY 241 RAD 243
DB 241 RAD 243

RESULT 5

AAR39569 standard; protein; 246 AA.

XX AAR39569;

XX 25-MAR-2003 (revised)

XX 07-FEB-1994 (first entry)

XX Sequence of 520C9 sFv protein.

XX Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;

XX biosynthetic single polypeptide chain binding site; ss.

XX Synthetic.

XX WO9316185-A2.

XX 19-AUG-1993.

XX 05-FEB-1993; 93WO-US001055.

XX 06-FEB-1992; 92US-00831967.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX (CENTU) CENTUS ONCOLOGY CORP.

PI Huston JS, Houston IL, Ring DB, Oppermann H;
XX WPI: 1993-272889/34.
DR N-PSDB; AA046084.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
XX
PS Claim 4; Page 60-61; 87pp; English.
XX
CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AA046083, AAR39568). A single chain Fv (scFv) is a covalently
CC linked VH-VL heterodimer which is expressed from a gene fusion including
CC VH- and VL- encoding genes connected by a peptide-encoding linker. Such
CC linker sequences are set forth in AA residues 116-135 in AAR39569, which
CC includes part of the 16 AA linker sequences in AAR39572. Using AA046084
CC for the 520C9 monoclonal antibody, a single chain polypeptide can be
CC produced having a binding affinity for a C-erbB-2 related antigen. 'X' in
CC AAR39569 refers to the location of a stop codon in AA046084. (Updated on
CC 25-MAR-2003 to correct PN field.)
CC
XX

Sequence 246 AA;

Query Match 100.0%; Score 1258; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 8, 9e-88;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVQSGPELKKRGEVYKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
DB 1 EIQLVQSGPELKKRGEVYKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
QY 61 ADPFKEFAFSLFETSAATHQINNLRNEDSATYFCARRRFGFAWGGTLVSVASISSS 120
DB 61 ADPFKEFAFSLFETSAATHQINNLRNEDSATYFCARRRFGFAWGGTLVSVASISSS 120
QY 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 180
DB 121 SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 180
QY 181 IYVTSGLDSGVKPRFSGSRGSDYSLTISSEDPVYVYCIQYAFPTTGGGNTLLEIK 240
DB 181 IYVTSGLDSGVKPRFSGSRGSDYSLTISSEDPVYVYCIQYAFPTTGGGNTLLEIK 240
QY 241 RAD 243
DB 241 RAD 243

RESULT 6
AAR39571
ID AAR39571 standard; protein; 534 AA.
XX
AC AAR39571;
XX
DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
DE Sequence of G-FIT.
XX
KM Tumour antigen; C-erbB-2; G-FIT.
XX
OS Synthetic.
XX
PN WO9316185-A2.
PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
XX
PR 06-FEB-1992; 92US-00831967.
XX

PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (CEU) Cetus ONCOLOGY CORP.
XX
XX Huston JS, Houston IL, Ring DB, Oppermann H;
XX WPI: 1993-272889/34.
DR N-PSDB; AA046086.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
XX
PS Example; Page 65-68; 87pp; English.
XX
CC C-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC cells, such as breast and ovarian tumour cells, which is an approx.
CC 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
CC 5.3 (see AA046083, AAR39568). (Updated on 25-MAR-2003 to correct PN
CC field.)
CC
XX

Sequence 534 AA;

Query Match 95.9%; Score 1206; DB 2; Length 534;
Best Local Similarity 95.1%; Pred. No. 2e-83;
Matches 233; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

QY 1 EIQLVQSGPELKKRPEYKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
DB 230 EIQLVQSGPELKKRPEYKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGQSTY 349
QY 61 ADPFKEFAFSLFETSAATHQINNLRNEDSATYFCARRRFGFAWGGTLVSVASISSS 120
DB 350 ADPFKEFAFSLFETSAATHQINNLRNEDSATYFCARRRFGFAWGGTLVSVASISSS 409
QY 121 --SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 178
DB 410 GGSGSGGSGSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIK 469
QY 179 RLIVATSLDSGVKPRFSGSRGSDYSLTISSEDPVYVYCIQYAFPTTGGGNTLLEIK 238
DB 470 RLIVATSLDSGVKPRFSGSRGSDYSLTISSEDPVYVYCIQYAFPTTGGGNTLLEIK 529
QY 239 IKRAD 243
DB 530 IKRAD 534

RESULT 7
AAU04945
ID AAU04945 standard; protein; 409 AA.
XX
AC AAU04945;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE Humanised anti-p185 antibody/IL-2 fusion protein.
XX
KM Humanised; antibody; p185, 520C9H; interleukin-2, IL-2; immunocongulate;
KM cancer; tumour; adenocarcinoma; fusion protein.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key
FH Peptide
FT 1..22
FT /label= Signal_peptide
FT 23..409
FT /label= Mature_fusion_protein
FT 23..259
FT Protein
FT /label= Humanised_antibody_520C9H
FT 53..57
FT Region

| | |
|---|--|
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Region | 72. .88 |
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Region | 121. .126 |
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Misc-difference | 123 |
| FT | /note= "Encoded by GCG" |
| Peptide | 138. .152 |
| FT | /label= Synthetic peptide linker |
| PT | /note= "Links the heavy chain to the light chain" |
| Region | 176. .186 |
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Region | 202. .208 |
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Region | 241. .249 |
| FT | /label= CDR |
| PT | /note= "Complementarity determining region" |
| Peptide | 261. .276 |
| FT | /label= Synthetic linker peptide |
| PT | /note= "Links the antibody to the IL-2 molecule" |
| Protein | 277. .409 |
| FT | /label= IL_2 |
| Misc-difference | 406 |
| FT | /note= "Encode by ACA" |
| PN | WO200153354-A2. |
| PD | 26-JUL-2001. |
| XX | |
| PE | 19-JAN-2001; 2001MO-US001919. |
| PR | 20-JAN-2000; 2000US-0177258P. |
| PA | (CHIR) CHIRON CORP. |
| PA | (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC. |
| PA | (HAMI-) HAMILTON REGIONAL CANCER CENT. |
| XX | |
| PI | Auretin R, Kwok CS, Ring DB; |
| DR | WPI; 2001-451904/48. |
| XX | N-PsDB; AAS09508. |
| PT | Novel immunconjugate useful for inhibiting tumor cell growth in vivo |
| PT | comprises a humanized anti-p185 antibody linked to an interleukin-2 |
| PT | polypeptide. |
| XX | |
| P8 | Claim 13; Fig 11; 74pp; English. |
| XX | |
| CC | The sequence represents a humanised anti-p185 (520C9) single chain |
| CC | antibody/human interleukin-2 (IL-2) fusion protein. The fusion protein |
| CC | (or immunoconguate) is used to inhibit the growth of tumours or cancers |
| CC | particularly those characterised by overexpression of p185 e.g. human |
| CC | adenocarcinomas and malignant and/or benign tumours of the breast, renal |
| CC | system, salivary gland, gastrointestinal tract or gastric tumours. |
| CC | (Updated on 06-AUG-2003 to correct OS field.) |
| XX | |
| SQ | Sequence 409 AA; |
| Query Match | 83.9%; Score 1055.5; DB 4; Length 409; |
| Best Local Similarity | 82.9%; Pred. No. 4,3e-72; |
| Matches 199; Conservative 19; Mismatches 19; Indels 3; Gaps 1 | |
| Ddb | 1 EIQLVQSPELTKPEETVVKISKASGYTPANGMMKCAPKGGLKMMWMINTYTGOSTY 60 |
| | 23 EIQLVQSEPVKKPPASVYKISKASGYTPANGMMKCAPKGGLKMMWMINTYTGOSTY 82 |
| Oy | 61 ADDEFKRFAPSLSTSATTAHLQINNLRNEDSATYFCARRFGFAYWGQTLVSASISS 120 |

| | | | |
|----------|--|---|-----|
| Db | 83 | ADDFKERTFTLIDTSTANHALEISLSRSDTDATYTCARRFGQAYWGGTLVTVS---SGS | 139 |
| Qy | 121 | SGSSSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGIKRL | 180 |
| Db | 140 | GGSGGGGGGGGGSDIQMTQSPSSLSASVQDRVLTLCRASQDIGNSLTWLQKRGKTIKRL | 199 |
| Qy | 181 | IYATSSLDGCVPKRRSGSRSGSDYSLTITSSLESDPFVVYVICQYAFPTTFGGGTULEIK | 240 |
| Db | 200 | IYATSSLDGCVPSRFGSGSRSGTDYTLTITSSLPEDPFVVYVICQYAFPTTFGGGTULEIK | 259 |
| RESULT 6 | | | |
| AAU72872 | | | |
| ID | AAU72872 | standard; protein; 499 AA. | |
| AC | AAU72872; | | |
| XX | 26-FEB-2002 | (first entry) | |
| DE | 3B10XP4-14 | bispecific single chain Fv. | |
| KM | Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; | | |
| KM | autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; | | |
| KM | intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; | | |
| KM | prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; DAPl0; | | |
| KM | sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPl0; | | |
| KM | hepatin; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7; | | |
| KM | 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14; | | |
| KM | P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14; | | |
| KM | P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23. | | |
| OS | Homo sapiens. | | |
| PN | WO20011005-A2. | | |
| XX | 27-SEP-2001. | | |
| XX | 26-MAR-2001; 2001WO-EP003414. | | |
| XX | 24-MAR-2000; 2000EP-00106467. | | |
| PA | (KUFEP/) KUFEP P. | | |
| PI | Kutler P, Riettmueller G, Luterduease R, Borschert K, Kischel R; | | |
| PI | Mayer M, Hofmeister R; | | |
| XX | WPI: 2002-055119/07. | | |
| XX | N-PSDB; AAS97146. | | |
| PT | Multifunctional polypeptides comprising binding sites that specifically | | |
| PT | recognize extracellular groups of the NKG2D receptor complex and domains | | |
| PT | which function as receptors or ligands, useful for treating cancers and | | |
| PT | infectious diseases. | | |
| PS | Example 5; Fig 16; 114pp; English. | | |
| XX | The invention relates to a multifunctional polypeptide comprising a | | |
| CC | domain with a binding site that specifically recognises an extracellular | | |
| CC | group of the NKG2D receptor complex and a second domain which functions | | |
| CC | as a receptor or ligand. The polypeptide and its associated | | |
| CC | polynucleotide are used for the preparation of a pharmaceutical | | |
| CC | composition for the treatment of cancer, infections and/or autoimmune | | |
| CC | conditions. The cancer may be a tumour of the head and neck, stomach, | | |
| CC | oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, | | |
| CC | larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, | | |
| CC | bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. | | |
| CC | The infectious diseases can be caused by viruses, bacteria, fungi, | | |
| CC | protozoa or helminths. The autoimmune diseases include multiple | | |
| CC | sclerosis, Grave's disease, ankylosing spondylitis, acute anterior | | |
| CC | uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent | | |
| CC | diabetes mellitus, Rheumatoid arthritis, pemphigus vulgaris and | | |
| CC | autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D | | |
| CC | receptor and the polypeptides of the invention | | |

```
XX Sequence 499 AA;
SQ
Query Match 77.6%; Score 976; DB 5; Length 499;
Best Local Similarity 55.1%; Pred. No. 6.1e-66;
Matches 199; Conservative 13; Mismatches 29; Indels 120; Gaps 1;

QY 1 EILVQSGPEIKKRGFTYKISCKASGYTFYFANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 128 QVQLQQSGPELKRGFTYKISCKASGYTFYFANYGNMNMKQAPGKGLKMGWINTYTGSEPTY 187
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 ADFKRRPAPSLFETSAATHLQINNLNEDSATYFCARRRGFAYWGQGTIVSASISSS 116
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 188 GDFKRGRAFSLFETSAATHLQINNLNEDSATYFCARRRGFAYWGQGTIVSASISSS 247
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 117 ----- 116
Db 248 EVQLLESGGGLVOPGGSLKLSCAASGFDPSRYSWVRQAAPGKGLIEWGINTPDSTINY 307
   117 -----ISSS 120
QY 308 TPSLKDKFTISRDNAAKNTLYIQMSKVRSEDTALYYCARGAVVAFEDYWGQGTIVVSSGG 367
   121 SSSSSSSSSSSGSDIQMTQSPSSLSASISGERVSLTCSRASODIGNSLTWLQOEPDGTIKRL 180
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 368 GSGSGSGSGSGSELVMTQSPSSLSASISGERVSLTCSRASODIGNSLTWLQOEPDGTIKRL 427
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 IYATSSLDGVPKRFSSRSGSDYSLTISLESDFVYVYCYOYAIFFPYFGGCTMLEIK 240
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 428 IYATSSLDGVPKRFSSRSGSDYSLTISLESDFVYVYCYOYAIFFPYFGGCTMLEIK 487
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 R 241
Db 488 R 488

RESULT 9
AAU04944
ID AAU04944 standard; protein; 267 AA.
XX
AC AAU04944;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE Humanised anti-p185 single chain antibody, 520C9H.
XX
KM Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunocjugate;
KM cancer; tumour; adenocarcinoma.
XX
OS Homo sapiens.
XX
OS Mus sp.
XX
OS Synthetic.
XX
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region /label= CDR
FT /note= "Complementarity determining region"
FT 72..88
FT /label= CDR
FT /note= "Complementarity determining region"
FT 121..126
FT /label= CDR
FT /note= "Complementarity determining region"
FT 138..152
FT /label= CDR
FT /note= "Complementarity determining region"
FT 176..186
FT /label= CDR
FT /note= "Complementarity determining region"
FT 202..208
FT /label= CDR
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FT /note= "Complementarity determining region"
FT Region 241..249
FT /label= CDR
FT /note= "Complementarity determining region"
FT 250..267
FT /label= Glu_Glu_epitope
XX
PN WO200153354-A2.
XX
PD 26-JUL-2001.
XX
PP 19-JAN-2001; 2001WO-US001919.
XX
PR 20-JAN-2000; 2000US-0177258P.
XX
PA (CHIR ) CHIRON CORP.
PA (HAMT-) HAMILTON CIVIC HOSPITALS RES DEV INC.
PA (HAMT-) HAMILTON REGIONAL CANCER CENT.
XX
PI Austen R, Kwok CS, Ring DB;
PI
XX
DR WPI; 2001-451904/48.
DR N-PSDB; AAS09507.
XX
PT Novel immunocjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an interleukin-2
PT polypeptide.
XX
PS Claim 7; Fig 9; 74pp; English.
XX
CC The sequence represents a humanised anti-p185 single chain antibody which
CC is linked to a human interleukin-2 (IL-2) molecule to make a fusion
CC protein. The fusion protein (or immunocjugate) is used to inhibit the
CC growth of tumours or cancers particularly those characterised by
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
CC benign tumours of the breast, renal system, salivary gland
CC gastrointestinal tract or gastric tumours. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 267 AA;

Query Match 75.6%; Score 950.5; DB 4; Length 267;
Best Local Similarity 71.6%; Pred. No. 2.5e-64;
Matches 174; Conservative 32; Mismatches 34; Indels 3; Gaps 1;

QY 1 EILVQSGPEIKKRGFTYKISCKASGYTFYFANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 23 EMQLVESGPEVKKRGASVAVKVSCKASGYTFYFANYGNMNMKQAPGKGLKMGWINTYTGQSTY 82
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 ADFKRRPAPSLFETSAATHLQINNLNEDSATYFCARRRGFAYWGQGTIVSASISSS 120
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 83 ADFKRRPAPSLFETSAATHLQINNLNEDSATYFCARRRGFAYWGQGTIVSASISSS 139
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 SSSSSSSSSSSGSDIQMTQSPSSLSASISGERVSLTCSRASODIGNSLTWLQOEPDGTIKRL 180
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 140 GSGSGSGSGSGSDIQMTQSPSSLSASISGERVSLTCSRASODIGNSLTWLQOEPDGTIKRL 199
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 IYATSSLDGVPKRFSSRSGSDYSLTISLESDFVYVYCYOYAIFFPYFGGCTMLEIK 240
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 200 IYATSSLDGVPKRFSSRSGSDYSLTISLESDFVYVYCYOYAIFFPYFGGCTMLEIK 259
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 RAD 243
   ::
Db 260 GSE 262

RESULT 10
AAW02278
ID AAW02278 standard; protein; 250 AA.
XX
AC AAW02278;
XX
DT 25-MAR-2003 (revised)
```

```

DT 29-OCT-1996 (first entry)
XX 741F8 anti-c-erbB-2 two single chain Fv construct.
XX
XX 741F8; anti-c-erbB-2; monoclonal antibody; single chain Fv; sfv;
KW construct; polypeptide linker; C-terminal amino acid sequence;
KW in vivo imaging; drug targeting experiment; homodimer; increased;
KW binding avidity; tissue retention time.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 122..135
XX /label= linker
XX Peptide 246..250
XX /note="Claimed C-terminal tail to facilitate
XX crosslinking of two sfv polypeptides"
XX
XX US5534254-A.
XX
XX 09-JUL-1996.
XX
XX 07-OCT-1993; 93US-00133804.
XX
XX 06-FEB-1992; 92US-00831967.
XX
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Opfermann H, Ring DB, Huston JS, Houston LL;
XX
XX WPI: 1996-333194/33.
XX N-PSDB; AAT36878.
XX
XX Compens. contg. antigen-targeting antibody fragment constructs -
XX comprising dimer of single-chain Fv fragments.
XX
XX Claim 25; Col 27-28; 30pp; English.
XX
XX The variable heavy (VH) and variable light (VL) genes of the 741F8 anti-c-
XX -erbB-2 monoclonal antibody (Mab), were isolated from the cDNA of the
XX parental 741F8 hybridoma line. A two single chain Fv (sfv) gene was
XX constructed by connecting the VH and VL genes with a DNA sequence
XX encoding a polypeptide linker. A synthetic DNA duplex encoding the C-
XX terminal amino acid sequence, (Gly)4-Cys was inserted, and the resulting
XX 741F8 anti-c-erbB-2 two sfv inserted into an expression vector. The
XX resulting gene, which encodes the present sequence, was transformed into
XX E. coli, and protein expression induced by the addn. of IPTG to the
XX culture medium. A compen. comprising a carrier and the 2 sfv protein
XX prod. can be used for in vivo imaging, and drug targeting experiments.
XX The 2 sfv protein prod. is a homodimer, in which both fragments target
XX the same antigen, therefore giving greater binding avidity and longer
XX tissue retention times, compared to individual sfv protein prod.
XX
XX CC fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 250 AA:
XX
XX Query Match 72.7%; Score 914; DB 2; Length 250;
XX Best Local Similarity 71.7%; Pred. No. 1.4e-61;
XX Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;
XX
XX 1 EIQVLOSGBELKPGGTIVKISCKASGYTPTANYGMNMKAPGKGLKMMKMTITTYGQSTY 60
DB 3 EIQVLOSGBELKPGGTIVKISCKASGYTPTNYGMNMVWKAPEGKGLKMMKMTINTTGEPTV 62
OY 61 ADDPKERFAPSLSTATTAHLQIINNCRNDSATYPCARF----GRAYVGGGTLVSVAS 116
DB 63 AEEFKGRFAPSLSTSTAYLQIINNKAEDTATYFCGRPFITTYGGRANNGGLTVTVA- 121
OY 117 ISSSSGSSSSSSSSGSDIQMTQSPSSLASLGERVSLTCRASQDIGNSLTWLQGEPPDGT 176
DB 122 -SSSSGSSSSSSSSS--SDIVMTQSPKFMSTVGDRAVSISCKASQDVSTAVAVYQKPGQS 178

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OY 177 IKRLIYATSSLDGVPKRPSSGRSGSDYSLTISLSSEDDFVVYVYQVLAIPYTFGCGTN 236
DB 179 PKLLIYMTSTRRTGVPDRFTSGSGSTDTLTISVQAEALAHYCOQHRYVRVTFGGGTR 238
OY 237 LEIKRAD 243
DB 239 LEIKRAD 245
OY
DB
RESULT 11
AAW29261
ID AAW29261 standard; protein; 250 AA.
XX
XX AAW29261;
XX
XX 25-MAR-2003 (revised)
XX 07-JAN-1998 (first entry)
XX
XX Anti-c-erbB-2 single chain antibody 741F8.
XX
XX Adenovirus; E1A; transactivator; transcription activator; stimulate;
KW expression vector; single-chain binding protein; VAI; enhance; PCR;
KW translation; production; immortal; eukaryotic cell; scfv; primer;
KW single-chain antibody fragment; imaging; tumour; breast cancer;
KW ovarian cancer; c-erbB-2 antigen; digoxin intoxication.
XX
XX OS Synthetic.
XX
XX US5658763-A.
XX
XX 19-AUG-1997.
XX
XX 05-JUN-1995; 95US-00463675.
XX
XX 25-OCT-1993; 93US-00143498.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Opfermann H, Dorai H;
XX
XX WPI: 1997-424235/39.
XX N-PSDB; AAT91837.
XX
XX Producing single chain binding protein in immortalised eukaryotic cells -
XX PT which comprise protein coding sequences, a transcription activator and
XX PT translation promotion sequences, provides high expression at low copy
XX number.
XX
XX Example 2; Col 29-32; 24pp; English.
XX
XX This sequence is a single chain anti-c-erbB-2 antibody (scfv) derived
XX CC from hybridoma 741F8. The protein product includes a C-terminal tail Gly4
XX CC -Cys in some constructs. Single-chain antibodies can be produced using a
XX CC novel method which comprises culturing an immortalised eukaryotic cell
XX CC having transfected DNA sequences (encoding the protein of interest),
XX CC integrated into its genome. In particular expression effector vectors
XX CC containing a non-native reporter DNA (encoding the scfv) and viral
XX CC sequences to promote transcription and translation (e.g. the adenovirus
XX CC E1A and VAI genes as shown in AAT91831 and AAT91834 respectively) are
XX CC used. The scfv that is produced, when properly folded, has a structure
XX CC with mono- or bi-functional binding activity. The method is especially
XX CC used to produce single-chain antibody fragments (scfv), e.g. for imaging
XX CC tumours or delivering therapeutic agents to them, particularly breast and
XX CC ovarian cancers that express the c-erbB-2 antigen. Other scfv are used in
XX CC model studies and for treating digoxin intoxication. (Updated on 25-MAR-
XX CC 2003 to correct PF field.)
XX
XX Sequence 250 AA:
XX
XX Query Match 72.7%; Score 914; DB 2; Length 250;
XX Best Local Similarity 71.7%; Pred. No. 1.4e-61;
XX Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;
XX

```


transcription activator protein. The cell allows the production on a commercial scale of proteins encoded by non-native hard to express genes

Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;
Best Local Similarity 71.7%; Pred. No. 1.4e-61;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVQSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60
DB 3 EIQLVQSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 62
QY 61 ADDEKRFAPSLFETSAATTAHLQINLRNEDSATYFCARF---GRAYVGGTIVSVSAS 116
DB 63 AEEFKGRFAPSLFETSAATTAHLQINLRNEDSATYFCARF---GRAYVGGTIVSVSAS- 121
QY 117 ISSSSGSSSSGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGSLTWLQOEPDGT 176
DB 122 -SSSSGSSSSGSSSS--SDIVMTQSPKFMSTVGDVRSISCKASQDVSTAVANYQOKPQGS 178
QY 177 IKRLIYATSSLDGVPKRFSGSRSGSDYSLTISLSESDPFVYYCLQYALFPYTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTGSGSGTDYTLTISVQAEIDLALHYCQGHYRVVYTFGGGTK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

RESULT 14

AAW53168
ID AAW53168 standard; protein; 250 AA.

AC AAW53168;
DT 16-JUL-1998 (first entry)

DE 741F8 anti-c-erbB-2 sfv' dimeric construct protein sequence.

KW Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer; c-erbB-2;
tumour; diagnosis.

OS Synthetic.
MUS Mus sp.

Key Location/Qualifiers
Peptide 122..135
/note="linker peptide"
Peptide 246..250
/note="Gly4-Cys C-terminal tail"

US5753204-A.

19-MAY-1998.

05-JUN-1995; 95US-00461838.

06-FEB-1992; 92US-00831967.

07-OCT-1993; 93US-00133804.

(CHIR) CHIRON CORP.

(CREA-) CREATIVE BIOMOLECULES INC.

WPI; 1998-311318/27.

N-PSDB; AAV21796.

Imaging of antigens in vivo - using dimers of single-chain antibody Fv fragments.

Example 1; Col 25-28; 30pp; English.

XX This represents the protein sequence of a 741F8 sfv' (single chain Fv) C-terminal Gly4-Cys construct. This was constructed by connecting the Vh and Vh genes with a DNA sequence encoding a 14 residue polypeptide linker. 741F8 is a monoclonal antibody useful in targeting c-erbB-2 antigen. This dimeric construct can be used in the method of invention of imaging a preselected antigen expressed in a mammal. The methods are used in magnetic resonance imaging of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic constructs have enhanced properties as in vivo targeting agents in comparison with intact monoclonal antibodies or their Fab fragments. The dimeric constructs permit the in vivo targeting of an epitope on an antigen with greater apparent avidity, including greater tumour specificity, tumour localisation and tumour retention properties than that of the Fab fragment having the same CDRS as the construct

Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;
Best Local Similarity 71.7%; Pred. No. 1.4e-61;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVQSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 60
DB 3 EIQLVQSGPELKKPGETVYKISCKASGYTFYFANYGMNMMKQAPGKGLKMMGMINTYTGQSTY 62
QY 61 ADDEKRFAPSLFETSAATTAHLQINLRNEDSATYFCARF---GRAYVGGTIVSVSAS 116
DB 63 AEEFKGRFAPSLFETSAATTAHLQINLRNEDSATYFCARF---GRAYVGGTIVSVSAS- 121
QY 117 ISSSSGSSSSGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGSLTWLQOEPDGT 176
DB 122 -SSSSGSSSSGSSSS--SDIVMTQSPKFMSTVGDVRSISCKASQDVSTAVANYQOKPQGS 178
QY 177 IKRLIYATSSLDGVPKRFSGSRSGSDYSLTISLSESDPFVYYCLQYALFPYTFGGGTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTGSGSGTDYTLTISVQAEIDLALHYCQGHYRVVYTFGGGTK 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

RESULT 15

AAW80422
ID AAW80422 standard; protein; 250 AA.

AAW80422;

28-JAN-1999 (first entry)

Anti-c-erbB-2 sfv' protein sequence.

Anti-c-erbB-2 sfv'; c-erbB-2; antigen; tumour cell; antibody 741F8;
targeted delivery; antigen-expressing cell.

OS Synthetic.
Homo sapiens.

Key Location/Qualifiers
Peptide 122..135
/note="linker"

US5837846-A.

17-NOV-1998.

05-JUN-1995; 95US-00461386.

06-FEB-1992; 92US-00831967.

07-OCT-1993; 93US-00133804.
(CREA-) CREATIVE BIOMOLECULES INC.

PA (CHIR) CHIRON CORP.

XX Oppermann H, Houston LL, Huston JS, Ring DB;

XX WPI; 1999-023541/02.

DR N-PSDB; AAV63397.

XX Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.

PS Example 1; Col 27-30; 29pp; English.

XX The present sequence represents an anti-c-erbB-2 sFv'. c-erbB-2 is an
CC antigen that is overexpressed on the surface of tumour cells. An antibody
CC designated 741F78 binds c-erbB-2. Variable heavy and light sequences of
CC antibody 741F8 are connected, together with a linker, to produce the
CC present single chain Fv gene. Anti-c-erbB-2 sFv' exemplifies the
CC invention. Dimers of the single chain Fv are used for targeted delivery
CC of drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium)
CC to antigen-expressing cells, particularly for treatment or diagnosis of
CC tumours (especially of ovary or breast)

XX Sequence 250 AA;

Query Match 72.7%; Score 914; DB 2; Length 250;

Best Local Similarity 71.7%; Pred. No. 1.4e-61;

Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

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QY 1 ETQLVSGPELKKPGRTVTKSCAKSGYTFANYGMNMKQAPGKGLKMGMINITYGOSTY 60
   |||
DB 3 ETQLVSGPELKKPGRTVTKSCAKSGYTFNYGMNMWKOAPGKGLKMGMININTGSEPTY 62
   |||
QY 61 ADDPKERFAFSLTSAATTAHLQINNLNEDSATYFCARRF---GFAVWGQGLTVSVSAS 116
   |||
DB 63 ABEFKRFRFAFSLTSAATTAHLQINNLNEDSATYFCARRF---GFAVWGQGLTVSVSAS 121
   |||
QY 117 ISSSSGSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQEPDGT 176
   |||
DB 122 -SSSSGSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQEPDGT 178
   |||
QY 177 IKRLIYATSLDGSVYKRFSGSRSGSDYSLTISLSEDPVYVYCYOYALFPTFGGGIN 236
   |||
DB 179 PKLLIYVSTRHGVDPRTGSGSGTDYTLTISVQAEIALHYCOQHRYRVPTFGGGITK 238
   |||
QY 237 LLEIKRAD 243
   |||
DB 239 LLEIKRAD 245

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Search completed: April 4, 2005, 15:47:05
Job time : 488.224 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 358.677 seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EQLVQSGPELKKRGETYKI.....YAIFFYTRGGTINLEIKRAD 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

1413372

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 1258 | 100.0 | 243 | 9 | US-09-887-853-6 |
| 2 | 1258 | 100.0 | 243 | 17 | US-10-683-547-6 |
| 3 | 1063.5 | 84.5 | 276 | 9 | US-09-766-543-12 |
| 4 | 976 | 77.6 | 499 | 15 | US-10-239-656-73 |
| 5 | 950.5 | 75.6 | 267 | 9 | US-09-766-543-10 |
| 6 | 914 | 72.7 | 250 | 9 | US-09-887-853-2 |
| 7 | 902 | 71.7 | 250 | 17 | US-10-683-547-2 |
| 8 | 861.5 | 68.5 | 236 | 17 | US-10-879-994-6 |
| 9 | 857.5 | 68.2 | 237 | 9 | US-09-924-099-9 |
| 10 | 857.5 | 68.2 | 243 | 9 | US-09-924-099-10 |
| 11 | 827 | 65.7 | 240 | 14 | US-10-127-890-148 |
| 12 | 827 | 65.7 | 240 | 17 | US-10-717-243-148 |
| 13 | 818 | 65.0 | 252 | 15 | US-10-239-656-55 |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 14 | 813.5 | 64.7 | 257 | 15 | US-10-239-656-67 | Sequence 67, Appl |
| 15 | 804 | 63.9 | 267 | 14 | US-10-071-485-2 | Sequence 2, Appl |
| 16 | 804 | 63.9 | 541 | 14 | US-10-071-485-85 | Sequence 85, Appl |
| 17 | 804 | 63.9 | 711 | 14 | US-10-071-485-90 | Sequence 90, Appl |
| 18 | 791.5 | 62.9 | 240 | 14 | US-10-071-485-91 | Sequence 91, Appl |
| 19 | 786 | 62.5 | 505 | 15 | US-10-239-656-79 | Sequence 79, Appl |
| 20 | 782.5 | 62.2 | 287 | 14 | US-10-222-026A-37 | Sequence 37, Appl |
| 21 | 782 | 62.2 | 503 | 15 | US-10-239-656-77 | Sequence 77, Appl |
| 22 | 779 | 61.9 | 235 | 14 | US-10-071-485-93 | Sequence 93, Appl |
| 23 | 766.5 | 60.9 | 230 | 14 | US-10-071-485-102 | Sequence 102, App |
| 24 | 766.5 | 60.9 | 248 | 10 | US-09-880-748-1104 | Sequence 1104, Ap |
| 25 | 766.5 | 60.9 | 248 | 15 | US-10-293-418-1104 | Sequence 1104, Ap |
| 26 | 764 | 60.7 | 251 | 10 | US-09-880-748-1921 | Sequence 1921, Ap |
| 27 | 764 | 60.7 | 251 | 15 | US-10-293-418-1921 | Sequence 1921, Ap |
| 28 | 764 | 60.7 | 503 | 15 | US-10-239-656-75 | Sequence 75, Appl |
| 29 | 762.5 | 60.6 | 248 | 10 | US-09-880-748-1446 | Sequence 1446, Ap |
| 30 | 762.5 | 60.6 | 248 | 15 | US-10-293-418-1446 | Sequence 1446, Ap |
| 31 | 743.5 | 59.1 | 248 | 10 | US-09-880-748-1778 | Sequence 1778, Ap |
| 32 | 743.5 | 59.1 | 248 | 15 | US-10-293-418-1778 | Sequence 1778, Ap |
| 33 | 740.5 | 58.9 | 250 | 10 | US-09-880-748-932 | Sequence 932, App |
| 34 | 740.5 | 58.9 | 250 | 15 | US-10-293-418-932 | Sequence 932, App |
| 35 | 735 | 58.4 | 895 | 16 | US-10-296-085A-19 | Sequence 19, Appl |
| 36 | 735 | 58.4 | 895 | 16 | US-10-296-085A-20 | Sequence 20, Appl |
| 37 | 735 | 58.4 | 895 | 16 | US-10-296-085A-27 | Sequence 27, Appl |
| 38 | 735 | 58.4 | 895 | 17 | US-10-496-179-4 | Sequence 4, Appl |
| 39 | 735 | 58.4 | 896 | 16 | US-10-296-085A-17 | Sequence 17, Appl |
| 40 | 735 | 58.4 | 896 | 16 | US-10-296-085A-18 | Sequence 18, Appl |
| 41 | 735 | 58.4 | 896 | 16 | US-10-296-085A-26 | Sequence 26, Appl |
| 42 | 735 | 58.4 | 896 | 17 | US-10-496-179-2 | Sequence 2, Appl |
| 43 | 735 | 58.4 | 896 | 17 | US-10-496-179-3 | Sequence 3, Appl |
| 44 | 735 | 58.4 | 896 | 17 | US-10-496-179-7 | Sequence 7, Appl |
| 45 | 735 | 58.4 | 899 | 16 | US-10-296-085A-28 | Sequence 28, Appl |

ALIGNMENTS

RESULT 1
US-09-887-853-6
Sequence 6, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
Oppermann, Hermann
Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/ Patent Department
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887, 853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133, 804
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 100.0%; Score 1258; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 7, 8e-86;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
DB 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
QY 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120
DB 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120
QY 121 SGGSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEEDGTIKRL 180
DB 121 SGGSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEEDGTIKRL 180
QY 181 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 240
DB 181 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 240
QY 241 RAD 243
DB 241 RAD 243

RESULT 2

US-10-683-547-6
Sequence 6, Application US/10683547
Publication No. US20050058638A1
GENERAL INFORMATION:
APPLICANT: Huston, J.
APPLICANT: Houston, L.L.
APPLICANT: Ring, D.
APPLICANT: Oppermann, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: CIBT-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 07/931,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 520C9 sFv
US-10-683-547-6

Query Match 100.0%; Score 1258; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 7, 8e-86;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
DB 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
QY 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120
DB 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120

DB 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120
QY 121 SGGSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEEDGTIKRL 180
DB 121 SGGSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEEDGTIKRL 180
QY 181 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 240
DB 181 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 240
QY 241 RAD 243
DB 241 RAD 243

RESULT 3

US-09-766-543-12
Sequence 12, Application US/09766543
Patent No. US20020041865A1
GENERAL INFORMATION:
APPLICANT: Austin, Richard
APPLICANT: Kwok, Cheuk S.
APPLICANT: Ring, David B.
TITLE OF INVENTION: METHODS FOR TREATING TUMORS
FILE REFERENCE: P01679, 002
CURRENT APPLICATION NUMBER: US/09/766,543
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/177,258
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 276
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus
US-09-766-543-12

Query Match 84.5%; Score 1063.5; DB 9; Length 276;
Best Local Similarity 83.3%; Pred. No. 2, 6e-71;
Matches 200; Conservative 19; Mismatches 18; Indels 3; Gaps 1;

QY 1 EIQLVSGPELKKRGEYTKISCKASGYTFPANYGNMNMKQAPGKGLKMGWINTYTGOSTY 60
DB 23 EIQLVSGPEVKKKGASVKISCKASGYTFPANYGNMNMKQAPGKLEMMGWINTYTGOSTY 82
QY 61 ADDPKERFAPSLFETSAITTAHLQINNLRNEDSATYFCARRFGFAYWGQGLTVSVASISSS 120
DB 83 ADDPKERPTFTLDISTTAHLFISLSSEDPYVYFCARRFGFAYWGQGLTVYS--SGG 139
QY 121 SGGSSSGSSSGSDIQMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQOEEDGTIKRL 180
DB 140 GSGSGSGSGSDIQMTQSPSSLSASVGDVRLTLCRASODIGNSLTWLQOEEDGTIKRL 199
QY 181 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 240
DB 200 IYATSSLDGVPKRRFGSGRSRGSYSLTISLSSEDPVYVYVCLOYAIFPYTFGGGTNLEIK 259

RESULT 4

US-10-239-656-73
Sequence 73, Application US/10239656
Publication No. US20040038339A1
GENERAL INFORMATION:
APPLICANT: KUPER, PETER
APPLICANT: RIETHMULLER, GERT
APPLICANT: LUTTERBUSE, RALF
APPLICANT: BOBSCHERT, KATRIN
APPLICANT: KISCHEL, ROMAN
APPLICANT: MAYER, MONIKA
APPLICANT: HOMMEISTER, ROBERT

;; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
;; FILE REFERENCE: 029976/0106
;; CURRENT APPLICATION NUMBER: US/10/239,656
;; CURRENT FILING DATE: 2003-03-06
;; PRIOR APPLICATION NUMBER: PCT/EP01/03414
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: EP 00106467.4
;; PRIOR FILING DATE: 2000-03-24
;; NUMBER OF SEQ ID NOS: 92
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 73
;; LENGTH: 499
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10XP4-
US-10-239-656-73
Query Match 77.6%; Score 976; DB 15; Length 499;
Best Local Similarity 55.1%; Pred. No. 1,6e-64;
Matches 199; Conservative 13; Mismatches 29; Indels 120; Gaps 1;
QY 1 BIQLVSGPELKKPGETVYKSCASGYTFANYGMNMKQAPGKGLKMGMINITYGQSTY 60
DB 128 QVQLQQSGPELKKPGETVYKSCASGYTFANYGMNMKQAPGKGLKMGMINITYGEPY 187
QY 61 ADFFKRFAPFSLFETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLVSVASIS 116
DB 188 GDDPFGRFAPFSLFETASATYVLIQINLNLRNEDTATYFCARRFPDPYWGQGLTVVSSGGGS 247
QY 117 ----- 116
DB 248 EVQLLESGGGLVQPGSLKSCAAGFDFSRVYMWKVRQAPGKGLIEWIGEINPDSSTNY 307
QY 117 ----- ISSS 120
DB 308 TPQLDKPFLSRDNKNTLYLQMSKVRSEDTALYYCARGAIVAPPYWGQGLTVVSSGG 367
QY 121 SSSSSSSSSSSGSDIQMTQSPPSLSASLGERVSLTCRASQDIGNSLTWLQEPDGTIKL 180
DB 368 GSGGGGGSGGGSELVMTQSPPSLSASLGERVSLTCRASQDIGNSLTWLQEPDGTIKL 427
QY 181 IYATSLDSGVPKRRSGSGSDYSLTISLSEDPFVYVYCCIQYAIFFYTFGGGTLLEIK 240
DB 428 IYATSLDSGVPKRRSGSGSDYSLTISLSEDPFVYVYCCIQYAIFFYTFGGGTLLEIK 487
QY 241 R 241
DB 488 R 488

;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: 520C9
;; OTHER INFORMATION: humanized single-chain antibody used in the
US-09-766-543-10
Query Match 75.6%; Score 950.5; DB 9; Length 267;
Best Local Similarity 71.6%; Pred. No. 6,4e-63;
Matches 174; Conservative 32; Mismatches 34; Indels 3; Gaps 1;
QY 1 BIQLVSGPELKKPGETVYKSCASGYTFANYGMNMKQAPGKGLKMGMINITYGQSTY 60
DB 23 EVQLVSGPEVKKPGASVYKSCASGYTFANYGMNMKQAPGKGLKMGMINITYGQSTY 82
QY 61 ADFFKRFAPFSLFETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLVSVASIS 120
DB 83 ADFFKRFAPFSLFETATTAHLQINLNLRNEDSATYFCARRFGPAYWGQGLVSVASIS 139
QY 121 SSSSSSSSSGSDIQMTQSPPSLSASLGERVSLTCRASQDIGNSLTWLQEPDGTIKL 180
DB 140 GSGGGGGSGGGSDIQMTQSPPSLSASVGDRTVITCRASQDIGNSLTWLQEPDGTIKL 199
QY 181 IYATSLDSGVPKRRSGSGSDYSLTISLSEDPFVYVYCCIQYAIFFYTFGGGTLLEIK 240
DB 200 IYATSLDSGVPRSRSGSGSDYSLTISLSEDPFVYVYCCIQYAIFFYTFGGGTLLEIK 259
QY 241 RAD 243
DB 260 GSE 262

RESULT 5
US-09-887-853-2
; Sequence 2, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; Oppermann, Hermann
; Houston, L. L.
; Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Tesca, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887, 853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133, 804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-887-853-2

Query Match 72.7%; Score 914; DB 9; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.1e-60;
Matches 177; Conservative 32; Mismatches 30; Indels 8; Gaps 3;

QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 60
DB 3 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 62
QY 61 ADDPKERPAFSLTSAITTAHLQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSAS 116
DB 63 AAEFKGRPAFSLTSAITTAHLQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSA- 121
QY 117 ISSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAWYQKPGQS 178
QY 177 IKRLIYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYICLQYALFPYTGCGTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTSGSGSDYTLTISVQAEIDLALHYCOQHRYKVPYTFGGGTX 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

RESULT 7
US-10-683-547-2
Sequence 2, Application US/10683547
Publication No. US20050058638A1

GENERAL INFORMATION:
APPLICANT: Huston, J. L.
APPLICANT: Houston, L. L.
APPLICANT: Ring, D.
APPLICANT: Oppermann, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: CIBT-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 07/831,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 250
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 741F8 sfv
US-10-683-547-2

Query Match 71.7%; Score 902; DB 17; Length 250;
Best Local Similarity 70.9%; Pred. No. 2.4e-59;
Matches 175; Conservative 32; Mismatches 32; Indels 8; Gaps 3;

QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 60
DB 3 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 62
QY 61 ADDPKERPAFSLTSAITTAHLQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSAS 116
DB 63 AAEFKGRPAFSLTSAITTAHLQINNLRNEDSATYFCARRF---GPAVWGQGLTVSVSA- 121
QY 117 ISSSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGT 176
DB 122 -SSSSSSSSSSSSSS--SDIWMQSPKFMSTSVGDVRSISCKASQDVSTAVAWYQKPGQS 178

QY 177 IKRLIYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYICLQYALFPYTGCGTN 236
DB 179 PKLLIYMTSTRHTGVDPDRFTSGSGSDYTLTISVQAEIDLALHYCOQHRYKVPYTFGGGTX 238
QY 237 LEIKRAD 243
DB 239 LEIKRAD 245

RESULT 8
US-10-879-994-6
Sequence 6, Application US/10879994
Publication No. US20050032175A1

GENERAL INFORMATION:
APPLICANT: Stahl, Neil
APPLICANT: Yancopoulos, George D.
APPLICANT: Katow, Margaret
APPLICANT: Smith, Eric
TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
FILE REFERENCE: REG 203E2
CURRENT APPLICATION NUMBER: US/10/879,994
CURRENT FILING DATE: 2004-06-29
PRIOR APPLICATION NUMBER: 10/610,452
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 236
TYPE: PRT
ORGANISM: homo sapiens
US-10-879-994-6

Query Match 68.5%; Score 861.5; DB 17; Length 236;
Best Local Similarity 69.7%; Pred. No. 2.3e-56;
Matches 168; Conservative 26; Mismatches 42; Indels 5; Gaps 2;

QY 1 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 60
DB 1 EIQLVOSGPELKKPGETYKISCKASGYTFANYGMNMWKAQPGKGLKMGMINITYGOSTY 60
QY 61 ADDPKERPAFSLTSAITTAHLQINNLRNEDSATYFCARRFPAVWGQGLTVSVSASISS 120
DB 61 NQKFRDAXATLVQDSTTAFAHNLNLTSEDSAVYFCAR--GURFWGQGLTVSVSA--CG 115
QY 121 SSSSSSSSSSSSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIRL 180
DB 116 GSGSGSGSGSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIRL 175
QY 181 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYICLQYALFPYTGCGTNLEIK 240
DB 176 IYATSSLDGVPKRRSGSGSDYSLTISLSEDFVYVYICLQYALFPYTGCGTNLEIK 235
QY 241 R 241
DB 236 R 236

RESULT 9
US-09-924-099-9
Sequence 9, Application US/09924099
Patent No. US20020128450A1

GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takao
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 9
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially produced peptide in the form of a single
OTHER INFORMATION: chain
OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18
US-09-924-099-9

Query Match 68.2%; Score 857.5; DB 9; Length 237;
Best Local Similarity 69.6%; Pred. No. 4.7e-56;
Matches 167; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

QY 1 EIQLVSGDELKPKGPTVYKISCKASGYTFANYGMNMMKAPKGLKMGNTYTGQSTY 60
DB 1 EIQLVSGDELKPKGASVAVSCASGYSTFDYFIYWKSHGKSLKEMICDIPYNGDTSY 60
QY 61 ADDPKERFAFSLETSATTAHLQINLNLRNEDSATYFCARRFGFAWYGQGLTVSVASISS 120
DB 61 NQKFRDKATLVYDQSTTAHMLNLSLSDSAVYFCAR--GLRFWQGLTVSVASG-GGG 117
QY 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 118 GSGGGGGSGGGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 177
QY 181 IYATSSLDGVPKRRFGSGRSRSGSDYSLTISLSEDPFVYVCLOVALPYTFGGGTNLK 240
DB 178 IYATSSLDGVPKRRFGSGRSRSGSDYSLTISLSEDPFVYVCLOVALPYTFGGGTNLK 237

RESULT 10

US-09-924-099-10
Sequence 10, Application US/09924099
Patent No. US20020128450A1
GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoohihiro
APPLICANT: OKURA, Takaochi
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 10
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially produced peptide in the form of a single
OTHER INFORMATION: chain
OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18
US-09-924-099-10

Query Match 68.2%; Score 857.5; DB 9; Length 243;
Best Local Similarity 69.6%; Pred. No. 4.8e-56;
Matches 167; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

QY 1 EIQLVSGDELKPKGPTVYKISCKASGYTFANYGMNMMKAPKGLKMGNTYTGQSTY 60
DB 1 EIQLVSGDELKPKGASVAVSCASGYSTFDYFIYWKSHGKSLKEMICDIPYNGDTSY 60

QY 61 ADDPKERFAFSLETSATTAHLQINLNLRNEDSATYFCARRFGFAWYGQGLTVSVASISS 120
DB 61 NQKFRDKATLVYDQSTTAHMLNLSLSDSAVYFCAR--GLRFWQGLTVSVASG-GGG 117
QY 121 SSSSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 180
DB 118 GSGGGGGSGGGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQOEPDGTIKRL 177
QY 181 IYATSSLDGVPKRRFGSGRSRSGSDYSLTISLSEDPFVYVCLOVALPYTFGGGTNLK 240
DB 178 IYATSSLDGVPKRRFGSGRSRSGSDYSLTISLSEDPFVYVCLOVALPYTFGGGTNLK 237

RESULT 11
US-10-127-890-148
Sequence 148, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Cartoll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mcandrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-10-127-890-148

Query Match 65.7%; Score 827; DB 14; Length 240;
Best Local Similarity 65.8%; Pred. No. 8.8e-54;


```
Db 61 TPLKDKFIIRSDNKNLTYLQMSKVRSDTALYCARGAVVAPFDYWGQTTVTS--- 117
Qy 118 SSSSSSSSSSSSSSSSDIOMTOSPSLSASLGERVSLTCRASODIGNSLTWLQOEPDGTI 177
Db 118 SGGGSGGGGSGGGGSELVMTQSPSLSLASLBERVSLTCRASODIGSSLMTWLOEPDGTI 177
Qy 178 KLIYATSLDSDGVPKRFSGRSGSDYSLTISLSESDFVYVYCIQYALFPTFGGNTL 237
Db 178 KLIYATSLDSDGVPKRFSGRSGSDYSLTISLSESDFVYVYCIQYALFPTFGGNTL 237
Qy 238 EIKR 241
Db 238 EIKR 241

RESULT 14
US-10-239-656-67
; Sequence 67, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOMMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239, 656
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-10 single
; US-10-239-656-67

Query Match 64.7%; Score 813.5; DB 15; Length 257;
Beet Local Similarity 64.7%; Pred. No. 9, 5e-53;
Matches 161; Conservative 33; Mismatches 44; Indels 11; Gaps 4;

Qy 1 EIQLV-QSGPELKPKPGETVYKISCKASGYTFANYGNMNMKQAPGKLMKMWINTYTGOST 59
Db 1 EYQLLEQSGALVVRGALVKLSCKASGFIKDYHVMWVKQRPQGLFWICWIDPENGMTI 60
Qy 60 YADDFKRFAPFSLFSTATTAAHQLINNLNEDSATYFCAR--RFGAY----WGQTIYS 112
Db 61 YDPKFGKASITADYTSNTAYLQISLSTSEDTAAAYCASFYYSYRFDVWGQTTVT 120
Qy 113 VASASISSSSSSSSSGSDIOMTOSPSLSASLGERVSLTCRASODIGNSLTWLQOE 172
Db 121 VS--SGGGSGGGGSGGGSELVMTQSPSLSLASLBERVSLTCRASODIGSSLMTWLOE 177
Qy 173 PDGTTIKRLIYATSLDSDGVPKRFSGRSGSDYSLTISLSESDFVYVYCIQYALFPTFG 232
Db 178 PDGTTIKRLIYATSLDSDGVPKRFSGRSGSDYSLTISLSESDFVYVYCIQYALFPTFG 237
Qy 233 GGTNLEIKR 241
Db 238 GGTNLEIKR 246
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```
RESULT 15
US-10-071-485-2
; Sequence 2, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071, 485
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485, 737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic
; US-10-071-485-2

Query Match 63.9%; Score 804; DB 14; Length 267;
Beet Local Similarity 63.8%; Pred. No. 5e-52;
Matches 155; Conservative 32; Mismatches 50; Indels 6; Gaps 3;

Qy 1 EIQLVQSGPELKPKPGETVYKISCKASGYTFANYGNMNMKQAPGKLMKMWINTYTGOSTY 60
Db 23 QYLVQSGSELKPKPASVYKISCKASGYTFIDYGNMNMVQAQGGKLMKMWINTYTGESTY 82
Qy 61 ADDEFKRFAPFSLFSTATTAAHQLINNLNEDSATYFCAR--RFGAYWGQTIYSVASIS 118
Db 83 VDDFKRFVPSLDTVSAAVYLQISLKAEDTATYFCARGFYAMDYWGQTTVTS---S 139
Qy 119 SSSSSSSSSSSSGSDIOMTOSPSLSASLGERVSLTCRASODIGNSLTWLQOEPDGTIK 178
Db 140 GGGGSGGGGSGGGSDIYLTQSPATMSASPERVTLTCSASSSI--SYMFVHQRPGQSPR 198
Qy 179 KLIYATSLDSDGVPKRFSGRSGSDYSLTISLSESDFVYVYCIQYALFPTFGGNTLE 238
Db 199 LIYDTSLMAGVPAKRFSGSGSTYSLLTISRMPEDEPATYFCHQSSSYPTFGQTKLE 258
Qy 239 IKR 241
Db 259 IKR 261
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Search completed: April 4, 2005, 16:42:42
Job time : 359.677 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 87.7284 seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-6

Perfect score: 1258

Sequence: 1 EIQLVQSGPELKKRGETYKI.....YAIFFYTRGGGNLEIKRAD 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 591.5 | 47.0 | 268 | 2 A56446 | Ig heavy chain V r |
| 2 | 571 | 45.4 | 249 | 2 S41374 | single chain Fv an |
| 3 | 521.5 | 41.5 | 146 | 4 S33905 | Ig heavy chain pre |
| 4 | 520.5 | 41.4 | 120 | 2 B42848 | I6 mb heavy chain |
| 5 | 517 | 41.1 | 136 | 2 S35759 | BHD9D10 protein - |
| 6 | 512 | 40.7 | 117 | 2 S32190 | Ig heavy chain V r |
| 7 | 510 | 40.5 | 119 | 2 A53285 | Ig heavy chain V a |
| 8 | 508 | 40.4 | 130 | 1 KVM5M4 | Ig heavy chain pre |
| 9 | 507 | 40.3 | 118 | 2 S19967 | Ig heavy chain V r |
| 10 | 505.5 | 40.2 | 115 | 2 S19968 | Ig heavy chain V r |
| 11 | 503.5 | 40.0 | 118 | 2 S37204 | Ig heavy chain V r |
| 12 | 501 | 39.8 | 233 | 2 UC5322 | p53 specific singl |
| 13 | 498 | 39.6 | 106 | 2 PL0260 | Ig kappa chain V r |
| 14 | 498 | 39.6 | 106 | 2 PL0259 | Ig kappa chain V r |
| 15 | 497.5 | 39.5 | 109 | 2 S26325 | Ig heavy chain V r |
| 16 | 497 | 39.5 | 113 | 2 B36259 | Ig heavy chain V r |
| 17 | 492 | 39.1 | 119 | 2 H45722 | anti-glycoprotein |
| 18 | 489 | 38.9 | 124 | 2 PH1404 | Ig heavy chain V r |
| 19 | 488 | 38.8 | 117 | 2 S32187 | Ig heavy chain V r |
| 20 | 487.5 | 38.8 | 115 | 2 S19965 | Ig heavy chain V r |
| 21 | 485.5 | 38.6 | 114 | 2 D32967 | Ig heavy chain V r |
| 22 | 475.5 | 37.8 | 114 | 2 C32967 | Ig heavy chain V r |
| 23 | 468.5 | 37.3 | 118 | 2 A32530 | Ig heavy chain V r |
| 24 | 468 | 37.2 | 106 | 2 PL0262 | Ig kappa chain V r |
| 25 | 466.5 | 37.1 | 139 | 2 PH1225 | Ig heavy chain pre |
| 26 | 462.5 | 36.8 | 120 | 2 S19963 | Ig heavy chain V r |
| 27 | 462 | 36.7 | 119 | 2 B32530 | Ig heavy chain V r |
| 28 | 456 | 36.2 | 105 | 2 S24765 | Ig heavy chain V r |
| 29 | 453 | 36.0 | 114 | 2 PL0256 | Ig heavy chain V r |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 447 | 35.5 | 108 | 4 B47271 | nitrophenyl phosph |
| 31 | 444 | 35.3 | 105 | 2 S24764 | Ig heavy chain V r |
| 32 | 433.5 | 34.5 | 101 | 2 D24672 | Ig heavy chain V r |
| 33 | 432 | 34.3 | 98 | 2 PH1062 | Ig light chain V r |
| 34 | 431 | 34.3 | 105 | 2 S24766 | Ig heavy chain V r |
| 35 | 423.5 | 33.7 | 120 | 2 S26789 | Ig heavy chain V r |
| 36 | 418.5 | 33.3 | 144 | 2 B30502 | Ig heavy chain V r |
| 37 | 418 | 33.2 | 134 | 2 S21916 | Ig heavy chain V r |
| 38 | 415 | 33.0 | 99 | 2 S26326 | Ig heavy chain V r |
| 39 | 415 | 33.0 | 105 | 2 S24763 | Ig heavy chain V r |
| 40 | 415 | 33.0 | 142 | 2 S19245 | Ig heavy chain pre |
| 41 | 413 | 32.8 | 88 | 2 PL0261 | Ig kappa chain V r |
| 42 | 412.5 | 32.8 | 93 | 2 C24672 | Ig heavy chain V r |
| 43 | 405 | 32.2 | 131 | 2 S26792 | Ig heavy chain V r |
| 44 | 404 | 32.1 | 129 | 2 D32513 | Ig kappa chain pre |
| 45 | 400 | 31.8 | 115 | 2 J10080 | Ig kappa chain pre |

ALIGNMENTS

RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A/Reference number: A56446; MUID:9522983; PMID:7713873

A/Accession: A56446

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 47.0%; Score 591.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 3e-35;

Matches 117; Conservative 46; Mismatches 75; Indels 7; Gaps 3;

| | | | |
|----|-----|---|-----|
| QY | 1 | EIQLVQSGPELKKRGETYKICKSGYTFANYGMNMQAPKQKXMGWITTYGQSY | 60 |
| DB | 3 | QVKIQESGAELVKKPQASVSLCTTSGFNIKDTYHWMVQRPPQGLEWIGRIAPANGITKY | 62 |
| QY | 61 | ADDFKRFAPSLTSAATTAHLQINNLRNEDSATYFCARRFPA--YWGQGLVSVSASI | 117 |
| DB | 63 | DPKIQGKATTAADTSNTATYQLSSLTSEDTNAYVCASYILRYENMGQITTVS--- | 119 |
| QY | 118 | SSSSGSSSSSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLQSPDGTI | 177 |
| DB | 120 | SGGGSGGGSDGGGSDIELTQSPAIMSASLGEKVTMCRASSV-NFIYWYQKSDASP | 178 |
| QY | 178 | KRLIYATSSLDGQVPRKRSRSGSDYSLTSSLSBDFVYCYCYALFPTTFGGTTL | 237 |
| DB | 179 | KLVVYVTHLPVGPVAPRSGSGNSYSLTSSMGEDAAATYCCQAFSSPTFGSTWL | 238 |
| QY | 238 | EIKRA 242 | |
| DB | 239 | EIKRS 243 | |

RESULT 2

S41374

single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

RESULT 10
S19968
Ig heavy chain V region (M-T408) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: S19968
R.Weissenborn, W.; Rietmueler, G.; Weiser, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A/Description: Structural characterization of CD4 mAb.
A/Reference number: S19963
A/Accession: S19968
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-115 <MOT>
A/Cross-references: UNIPROT:Q921A6, EMBL:X65089
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P.10-93/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 505.5; DB 2; Length 115;
Best Local Similarity 80.9%; Pred. No. 1.6e-29;
Matches 93; Conservative 8; Mismatches 9; Indels 5; Gaps 1;
QY 6 QSGPELKKPGETVTKISCKASGYTPFANYGMNMMKQAPGKGLKMMGINTNTYGSTYADDFK 65
DB 1 QSGPELTKPGETVTKISCKASGYTPFANYGMNMMKQAPGKGLKMMGINTNTYGSTYADDFK 60
QY 66 ERPAFSLFETSAITTAHLQINNLNEDSATYFCAR----RFQFAYWGGTLVSVA 115
DB 61 GRPAFSLFETSAITTAHLQINNLNEDSATYFCARGPYPYRSPYWGQTLTVSS 115

RESULT 11
S37204
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C/Accession: S37204
R.Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, V.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S37204
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <FIS>
A/Cross-references: EMBL:X74589; NID:g402599; PIDD:CA52666.1; PID:g1333981
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
P.15-98/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 503.5; DB 2; Length 118;
Best Local Similarity 79.8%; Pred. No. 2.2e-29;
Matches 95; Conservative 12; Mismatches 7; Indels 5; Gaps 2;
QY 1 EILVVSQPELKKPGETVTKISCKASGYTPFANYGMNMMKQAPGKGLKMMGINTNTYGSTY 60
DB 1 QILVVSQPELKKPGETVTKISCKASGYTPIDYSMHVVKQVPGKGLKMMGINTNTGEAKY 60
QY 61 ADDFKRPAFSLFETSAITTAHLQINNLNEDSATYFCARFG---FAVWGQTLVSVA 115
DB 61 ADDFKRPAFSLFETSAITTAHLQINNLNEDSATYFCAR-FWGSAMFPYWGQTLTVSA 118

RESULT 12
JCS322
p53 specific single-chain antibody Pab421 - human
C/Species: Homo sapiens (man)
C/Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C/Accession: JCS322
R.Jaennot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A/Reference number: JCS322; MUID:97168950; PMID:9016757

A/Accession: JCS322
A/Molecule type: mRNA
A/Residues: 1-233 <JAN>
A/Experimental source: hybridoma cell
C/Comment: This protein specifically binds the tumor suppressor protein p53. It restores
Query Match 39.8%; Score 501; DB 2; Length 233;
Best Local Similarity 43.3%; Pred. No. 7.3e-29;
Matches 103; Conservative 46; Mismatches 79; Indels 10; Gaps 4;
QY 6 QSGPELKKPGETVTKISCKASGYTPFANYGMNMMKQAPGKGLKMMGINTNTYGSTYADDFK 65
DB 2 ESGAEILVRSQAVKSLCTSGFNINDYHMHVKKRPEQGLEIGRIDPENGADMTRSSG 61
QY 66 ERPAFSLFETSAITTAHLQINNLNEDSATYFCARRRFPAYWGGTLVSVA81SSSSGSS 125
DB 62 VAAITMTADTSSNTATVQLQSLTSEDTAVYYC--NAGMDYWGQTLVYS---SGGSGSG 116
QY 126 SGSSSSGSDIQMTQSPSSLSASLGERVSLTCRASQDIGNS----LTWLOQEPDGTIKRLI 181
DB 117 RASGGGSGSDIELTQSPASLAVSLGQRAVISCRAKSVSTSGVYHMMNQKPGPRLII 176
QY 182 YATSSLDGVPKRRFGSGSDYSLTSSLSSEDFVYVCLOVAFPYTFGGTNLEI 239
DB 177 YIVSNLESQVPAFRFGSGSGDTFTLNIHPVEEDAAATYYC-QHIRELTRSGGTLEI 233

RESULT 13
PL0260
Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: PL0260
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0260
A/Molecule type: mRNA
A/Residues: 1-106 <SHL>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P.1-23/Region: framework 1
P.16-90/Domain: immunoglobulin homology <IMM>
P.124-34/Region: complementarity-determining 1
P.135-49/Region: framework 2
P.150-56/Region: complementarity-determining 2
P.157-88/Region: framework 3
P.189-97/Region: complementarity-determining 3
P.198-106/Region: framework 4

Query Match 39.6%; Score 498; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 4.9e-29;
Matches 99; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 134 DIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLOQEPDGTIKRLIATSSLDGVPK 193
DB 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGNSLTWLOQEPDGTIKRLIATSSLDGVPK 60
QY 194 RFGSGRSGSDYSLTSSLSSEDFVYVCLOVAFPYTFGGTNLEI 239
DB 61 RFGSGRSGSDYSLTSSLSSEDFVYVCLOVAFPYTFGGTNLEI 106

RESULT 14
PL0259
Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: PL0259
R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0259
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 39.6%; Score 498; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 4.9e-29;
Matches 99; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 134 DIQMTQSPESLSASISGERYSLTCSRASODIGNSLTWLQEPDGTIKRLIYNTSSLDGVPK 193
DB 1 DIQMTQSPESLSASISGERYSLTCSRASODIGNSLTWLQEPDGTIKRLIYNTSSLDGVPK 60

QY 194 RFGSGRSGSDYSLTSSLESDFFVYVYCIQYAIFFPYTFGGTNIET 239
DB 61 RFGSGRSGSDYSLTSSLESDFFVYVYCIQYATSPWTFGGTNIET 106

RESULT 15
S26325
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26325
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:952080; PID:g1334043
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocetramer; immunoglobulin
F:5-88/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 497.5; DB 2; Length 109;
Best Local Similarity 85.3%; Pred. No. 5.5e-29;
Matches 93; Conservative 7; Mismatches 4; Indels 5; Gaps 2;

QY 11 LKKPGETVXISCKASGYTFANYGMNMKQAPGKGLKMGMINYYTGOSTYADDFKRFAPF 70
DB 1 LKKPGETVXISCKASGYTFANYGMNMVKAAPGKGLKMGMINYYTGEPYADDFKRFAPF 60

QY 71 SLETSATTAHLQINLRNEDSATYFCAR---RF-GPATWGQGTIVSVS 114
DB 61 SLETSASTAYLQINLRNEDMATYFCARPAYRYDGFAYWGQGTIVTVS 109

Search completed: April 4, 2005, 15:57:59
Job time : 89.7284 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 410.693 Seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-6
Perfect score: 1258
Sequence: 1 EQLVQSGPELKKPEETVKI.....YAIFFYTGCGTNEIKRAD 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_prot: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 827.5 | 65.8 | 241 | 2 | Q92IA6 mus musculu |
| 2 | 737.5 | 58.6 | 244 | 2 | Q65ZC8 mus musculu |
| 3 | 690.5 | 54.9 | 240 | 2 | Q65ZC9 mus musculu |
| 4 | 661 | 52.5 | 218 | 2 | Q925S1 mus musculu |
| 5 | 636.5 | 50.6 | 243 | 2 | Q7QWM2 mus musculu |
| 6 | 636 | 50.6 | 298 | 2 | Q6QYF0 mus musculu |
| 7 | 628.5 | 50.0 | 487 | 2 | Q65ZL2 mus musculu |
| 8 | 618.5 | 49.2 | 255 | 2 | Q6KB05 mus musculu |
| 9 | 590 | 46.9 | 248 | 2 | Q65ZQ7 mus musculu |
| 10 | 517 | 41.1 | 484 | 2 | Q92IA6 mus musculu |
| 11 | 508 | 40.4 | 130 | 1 | KV5G MOUSE |
| 12 | 492 | 39.1 | 127 | 2 | Q925S9 mus musculu |
| 13 | 470.5 | 37.4 | 116 | 2 | Q683Y7 mus musculu |
| 14 | 458.5 | 36.4 | 140 | 2 | Q65ZL3 mus musculu |
| 15 | 436 | 34.7 | 102 | 2 | Q9JL79 mus musculu |
| 16 | 421.5 | 33.5 | 116 | 2 | Q683Y8 mus musculu |
| 17 | 394 | 31.3 | 108 | 1 | KV5J MOUSE |
| 18 | 393 | 31.2 | 107 | 2 | Q9JL84 mus musculu |
| 19 | 392 | 31.2 | 108 | 1 | KV5M MOUSE |
| 20 | 389 | 30.9 | 108 | 1 | KV1R HUMAN |
| 21 | 389 | 30.9 | 108 | 1 | KV5L MOUSE |
| 22 | 389 | 30.9 | 108 | 1 | KV5O MOUSE |
| 23 | 388 | 30.8 | 108 | 1 | KV5N MOUSE |
| 24 | 386 | 30.7 | 108 | 1 | KV5K MOUSE |
| 25 | 385 | 30.6 | 236 | 2 | Q6GMX3 mus musculu |
| 26 | 384 | 30.5 | 236 | 2 | Q7TS98 mus musculu |
| 27 | 377 | 30.0 | 480 | 2 | Q6R0Z4 mus musculu |
| 28 | 375.5 | 29.8 | 614 | 2 | Q7TMT6 mus musculu |
| 29 | 373.5 | 29.7 | 125 | 2 | Q6PIL0 mus musculu |
| 30 | 373.5 | 29.7 | 500 | 2 | Q6N091 mus musculu |
| 31 | 371 | 29.5 | 117 | 1 | KV5H MOUSE |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 32 | 370.5 | 29.5 | 481 | 2 | OBVCV5 mus musculu |
| 33 | 369 | 29.3 | 108 | 1 | KV5U MOUSE |
| 34 | 369 | 29.3 | 236 | 2 | Q6GMW1 mus musculu |
| 35 | 369 | 29.3 | 236 | 2 | Q723Y4 mus musculu |
| 36 | 364 | 28.9 | 236 | 2 | Q6GMX8 mus musculu |
| 37 | 364 | 28.9 | 498 | 2 | Q6N041 mus musculu |
| 38 | 363 | 28.9 | 236 | 2 | Q6GMX0 mus musculu |
| 39 | 363 | 28.9 | 488 | 2 | Q91WR1 mus musculu |
| 40 | 362 | 28.8 | 123 | 2 | Q8V1J1 mus musculu |
| 41 | 361.5 | 28.7 | 481 | 1 | Q91WT1 mus musculu |
| 42 | 361 | 28.7 | 108 | 1 | KV1G HUMAN |
| 43 | 361 | 28.7 | 108 | 2 | Q9UL70 mus musculu |
| 44 | 361 | 28.7 | 128 | 1 | KV5E MOUSE |
| 45 | 360 | 28.6 | 108 | 1 | KV1Y HUMAN |

ALIGNMENTS

| | | | | | |
|--|--|---|-----|-------|-------------------------|
| RESULT 1 | | | | | |
| Q92IA6 | PRELIMINARY; | PRT; | 241 | AA. | |
| AC | Q92IA6; | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | | |
| DT | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | | |
| DE | Anti-CBA 79 single chain Fv (fragment). | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_Taxid=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | MEDLINE=98170165; PubMed=9509426; | | | | |
| RA | Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., | | | | |
| RA | Yi K.S., Suh P.G., Ryu S.H., Chung H.K.; | | | | |
| RT | "Cloning and characterization of cDNAs encoding VH and VL of a | | | | |
| RT | monoclonal anti-CBA antibody (CBA 79) cross-reactive with NCA-95 and | | | | |
| RT | generation of a single-chain Fv molecule (scFv)."; | | | | |
| RL | Mol. Cells 7:816-819(1997). | | | | |
| DR | EMBL, U88067; ABA8044.1; -. | | | | |
| DR | PIR, S19965; S19965. | | | | |
| DR | PIR, S19967; S19967. | | | | |
| DR | PIR, S19968; S19968. | | | | |
| DR | PIR, S26325; S26325. | | | | |
| DR | HSSP; P01607; 1BMW. | | | | |
| DR | SMART; SM00406; IGV; 2. | | | | |
| DR | PROSITE; P850835; IG_LIKE; 2. | | | | |
| FT | NON_TER | | | | |
| FT | NON_TER | | | | |
| FT | NON_TER | | | | |
| SQ | SEQUENCE | 241 | AA; | 26086 | MM; |
| | | | | | 0276887248E9C771 CRC64; |
| Query Match | | | | | |
| Score 827.5; DB 2; Length 241; | | | | | |
| Best Local Similarity 65.4%; Pred. No. 3.9e-58; | | | | | |
| Matches 161; Conservative 27; Mismatches 49; Indels 9; Gaps 4; | | | | | |
| QY | 1 | EQLVQSGPELKKPEETVKISKASGYTFPANYGMNMKQAPKGLKMGWINTYTGQSTY | 60 | | |
| | ::: | | ::: | | ::: |
| DB | 1 | QVKLQSGPELKKPEETVKISKASGYTFDYGMMWVQAPKGLKMGWINTYTGEPY | 60 | | |
| QY | 61 | ADDFKERRAFSLFETATTAHLQINLKNEDSAITTYCAR--- | 116 | | |
| | ::: | | ::: | | ::: |
| DB | 61 | ADDFKERRAFSLFETATTAHLQINLKNEDSAITTYCAR--- | 117 | | |
| QY | 117 | ISSSSGSSSSGSSSSGSIOMTQSPSSLASLGEVSLTCRASQDIGNSLTWIQGPEDT | 176 | | |
| | ::: | | ::: | | ::: |
| DB | 118 | -SGGSGSSGSSGSSGSSIBLTQSSLSASLGGAVTTTCRASQDINKYIAHYQKPKG | 176 | | |
| QY | 177 | IKRLIYATSSLDGVPKPFSGSGSDYSLRTISSLESDPVVYVYCLQYAIFFYTGCGTN | 236 | | |
| | ::: | | ::: | | ::: |
| DB | 177 | PRSAHTLIYIOPGIPSRFSGSGSDYSLRTISSLESDPVVYVYCLQYAIFFYTGCGTK | 235 | | |
| QY | 237 | LEIKRA 242 | | | |

Db 236 LELKRA 241

RESULT 2

065ZC8 PRELIMINARY; PRT; 244 AA.

AC 065ZC8; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Single-chain Fv (Fragment).
 Name=scfv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 GN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97362799; PubMed=9219263;

RA Kontermann R.E., Wing M.G., Winter G.;

RT "Complement recruitment using bispecific diabodies.";

RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL; Y13057; CA73500.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PS50835; IG_LIKE; 2.

FT NON TER 1

FT NON TER 244

SO SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 58.6%; Score 737.5; DB 2; Length 244;

Best Local Similarity 55.5%; Pred. No. 6, 1e-51;

Matches 137; Conservative 47; Mismatches 54; Indels 9; Gaps 2;

QY 1 EIQLVQSGPELKKRGERTVTKISCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
 Db 1 QVQLVQSGAEVKKPQDSVKVSCASGTFPSDHYMHWYRQAPGGLEMGWINDPNDTRF 60
 QY 61 ADDPKERFAPSLTSAATTAHLQINNLNEDSATYFCARR-----FGFAYWGQGLVSVS 114
 Db 61 AGRFQGVVTWTRDPTISAAVMEVSRRLRSDPLAVYYCARFGTSALIGMHWGQGLVTVS 120
 QY 115 ASISSSSSSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQEPD 174
 Db 121 ---SGGGSGGGSGGGSDIOMTQSPSTLSASIGDRVITCRASGIGHYMLAWYQKPG 177
 QY 175 GTRKRLIYATSSLDGCVPKRPSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGG 234
 Db 178 KAPKFLIYKASSLSASAPSRFSSSGTPTLTLSLQPDPAFYTCQQYSNYPPLFGGG 237
 QY 235 TNLKTR 241
 Db 238 TKLEIKR 244

RESULT 3

065ZC9 PRELIMINARY; PRT; 240 AA.

AC 065ZC9; 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Single-chain Fv (Fragment).
 Name=scfv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

EN [1]
 RP SEQUENCE FROM N.A.

RX STRAIN=C1q/7;

RX MEDLINE=97362799; PubMed=9219263;

RA Kontermann R.E., Wing M.G., Winter G.;

RT "Complement recruitment using bispecific diabodies.";

RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL; Y13056; CA73499.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PS50835; IG_LIKE; 2.

FT NON TER 1

FT NON TER 240

SO SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 54.9%; Score 690.5; DB 2; Length 240;

Best Local Similarity 55.6%; Pred. No. 3, 4e-47;

Matches 135; Conservative 40; Mismatches 63; Indels 5; Gaps 2;

QY 1 EIQLVQSGPELKKRGERTVTKISCKASGYTFANYGNMNMKQAPGKGLKMGWINTYTGQSTY 60
 Db 1 QVQLVQSGGLVQPGGSLRLCAASGTFSSYGMHWYRQAPGKGLFWAVSYDGSNKYY 60
 QY 61 ADDPKERFAPSLTSAATTAHLQINNLNEDSATYFCARRFGFAV--WGQGLVSVASIS 118
 Db 61 ADVYKGRFTIRSDNSKNTLYQMSLRADTAAYVYCARMDGSDLPWGKGLTVS--S 117
 QY 119 SSSGSSSSSSSSSDIOMTQSPSSLSASLGERVSLTCRASODIGNSLTWLQEPDGTIK 178
 Db 118 GGGSGGGSGGGSDIOMTQSPSTLSASIGDRVITCRASGIGHYMLAWYQKPGAPK 177
 QY 179 RLIVATSSLDGCVPKRPSGSGSDYSLTISLSEDFVYVYCLQYALFPTFGGGTNLE 238
 Db 178 LLIKYASSLSRAPSRFSSGSGTPTLTLSLQPDPAFYTCQQYSNYPPLFGGGTKLE 237
 QY 239 IKR 241
 Db 238 IKR 240

RESULT 4

0925S1 PRELIMINARY; PRT; 218 AA.

AC 0925S1; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE MRP5 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 GN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL: AF240168; AAK43733.1; -.
DR HSP; P01665; 10WZ.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match 52.5%; Score 661; DB 2; Length 218;
Best Local Similarity 58.9%; Pred. No. 6.9e-45;
Matches 129; Conservative 32; Mismatches 48; Indels 10; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMKQAPGKGLKMKGMINTYTGQSTY 60
DB 3 QVXKQSGPELKKPEETVYKISCKASGYTTTGMQMVQCMQPKGLKMKGMINTHSGVPRX 62
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNDSATYFCAR--RFGPAYWGQGLTVSVASIS 117
DB 63 AEEFKGRFAPFSLTETASTAYLQISNLKNEDTATYFCMRWDYDGGFAYWGQGLTVTVS--- 119
QY 118 SSSSGSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGN---SLTWLQOEP 173
DB 120 SGGSGSGSGSGSDIVLTQSPASLAVSLQORATISCRASGSVDNIGISFMNWFQOKP 179
QY 174 DGTIKRLIYATSLDSGVKPRFSGRSRGSQDYSLTISLRE 212
DB 180 GQPKLLIYNAKQSGSVAGLLAGSGSGTDFSLNITPME 218

RESULT 5

Q7TQM2 PRELIMINARY; PRT; 243 AA.

AC 07TQM2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN Name=SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C.
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Etteharta P., Billiald P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAB00495.1; -.
DR HSP; P01751; 1A6W.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 50.6%; Score 636.5; DB 2; Length 243;
Best Local Similarity 52.3%; Pred. No. 7.1e-43;
Matches 126; Conservative 43; Mismatches 67; Indels 5; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMKQAPGKGLKMKGMINTYTGQSTY 60
DB 1 QVQLQSGSELVVRPQASVTLSCASGYTFYTMHVMVKQRHQGLEWIGINIVPGSITNY 60
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNDSATYFCAR--RFGPAYWGQGLTVSVASIS 119
DB 61 DEKFNKGLIYVDTSSITAYMHLSSLASDSDAVYTCARGRGLDVGAGITTLTVS--SG 117
QY 120 SSSSGSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTIR 179
DB 118 GGGSGSGSGSGSDIQMTQSSSSPSVSLGVDVITITCKASEDIYNRLANYQOKPGNAPRL 177

QY 160 LIYATSLDSGVKPRFSGRSRGSQDYSLTISLSEDPFVYVYCLQYAIPTFTGGGTNLREI 239
DB 178 LISGATSLTGVPSRFSRSGSGKYTLTSLQTDVATYVCOQY-WSTRTRGGGKXLEI 236
QY 240 K 240
DB 237 K 237

RESULT 6

Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name=CN 8 scFv;
OS synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_TaxId=32630;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phase display subtraction
method";
RT Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
RL EMBL; AB036341; BAA86833.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSP; P01820; 1A7O.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F968BA17004317 CRC64;

Query Match 50.6%; Score 636; DB 2; Length 298;
Best Local Similarity 51.4%; Pred. No. 1e-42;
Matches 126; Conservative 42; Mismatches 71; Indels 6; Gaps 3;

QY 1 EIQLVQSGPELKKPEETVYKISCKASGYTFANYGMNMKQAPGKGLKMKGMINTYTGQSTY 60
DB 40 QVQLQSGGGLVYKPGSGLKLSCAASGSDFSRYMGMVVRQAPGKGLIEWIGINIPDSSTINY 99
QY 61 ADDEKRFAPFSLTETATTAHLQINNLRNDSATYFCAR--RFG--AYWGQGLTVSVASIS 117
DB 100 TPSLKDKFTISRDNKNTLYLQMSKVRSEDTALVYTCARASYGHSAYWGQGLTVTVS--- 156
QY 118 SSSSGSSSSSSSGSDIQMTQSPSLASLGERVSLTCRASQDIGNSLTWLQOEPDGTI 177
DB 157 SGGSGSGSGSGSDIELTQSPASLAVSLQORATISCRASGSVDNIGISFMNWFQOKP 216
QY 178 KRLIYATSLDSGVKPRFSGRSRGSQDYSLTISLSEDPFVYVYCLQYAIPTFTGGGTNL 237
DB 217 QLVVNAKTLADGVPSRFSRSGSGTQYSLKINSIQPEDFGSYCQHFMTTPTFTGGGTNL 276
QY 238 EIKRA 242
DB 277 EIKRA 281
RESULT 7
Q6SZL2 PRELIMINARY; PRT; 487 AA.
AC Q6SZL2;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE FV/M4.

GN Name=M4-IPN-<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y. Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
antibody secreted from myeloma cells."
RL Hum. Antibodies Hydrindomas 6:161-166 (1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR003598; IG_2.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG_3.
DR SMART; SM00407; IG_1; 2.
DR SMART; SM00408; IG_2; 2.
DR SMART; SM00406; IG_V; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 487 AA; 53578 MW; C7EAB69F30555504 CRC64;

Query Match 50.0%; Score 629.5; DB 2; Length 487;
Best Local Similarity 50.8%; Pred. No. 6.1e-42;
Matches 122; Conservative 46; Mismatches 67; Indels 5; Gaps 2;

QY 1 EIQLVSGPELKKPGETVTKISCKASGYTPANYGMNMMKQAPGKGLKMGWINTYTGSTY 60
DB 20 QVQLQQSGDDELVPKSGSVKISCKASGYTFTDTHAIHMAKQPEQGLMIGVTSFGNDIKY 79
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRFPAYWGQGLTVSVASIS 120
DB 80 NEKFKKATLTADKSSSTAVMQLNSLTSDSAVYFCRRY-YHWQGGTTLTG---SGG 134
QY 121 SGSSSSGSSSGSDIQMTQSPSLSLASLGERVSLTCRASQDIGNSLTWLQSPDGTIKRL 180
DB 135 GSGGGGSGSGSGSRIMTQSPSLSVSVGLVLTTCRASENIYSNLAWYQKQKSGSPQL 194
QY 181 IYATSLDGVPRKPRFSGSRGSDYSLTISLSEDPVYVYCCQYALPFTTREGGNTLEIK 240
DB 195 VYATNLADGVPRKPRFSGSGSDYSLTISLSEDPGSIYCOHFWGTPYTFGGGTRLEIK 254

RESULT 8

Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCFV B8E5 protein (Fragment).
GN Name=scfv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; F01837; 1KCR.
DR InterPro; IPR003599; IG_
DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IG_2.
DR SMART; SM00406; IG_V; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 49.2%; Score 618.5; DB 2; Length 255;
Best Local Similarity 48.0%; Pred. No. 2.1e-41;
Matches 121; Conservative 46; Mismatches 70; Indels 15; Gaps 3;

QY 1 EIQLVSGPELKKPGETVTKISCKASGYTPANYGMNMMKQAPGKGLKMGWINTYTGSTY 60
DB 1 QVQLQQSGDDELVPKSGSVKISCKASGYTFTDTHAIHMAKQPEQGLMIGVTSFGNDIKY 79
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRFPAYWGQGLTVSVAS 114
DB 61 PDVKGRTTISRDNKNTLYLQMSLSLSEDPYVYCAHINRYDGAIDYGGTTLTVS 120
QY 115 ASISSSGSSSGSSGSDIQMTQSPSLSLASLGERVSLTCRASQDIGNSLTWLQSPDGT 168
DB 121 ---SGGGSGSGSGSDIYMAQSPSLSVSAGEKVMSCSKSQSLNLRNQNYLAW 177
QY 169 LQSPDGTIKRLIYATSLDGVPRKPRFSGSRGSDYSLTISLSEDPVYVYCCQYALP 228
DB 178 YQKRGQSPKLLIYASTRESGVPDRFTGSGSDYFTLISVQAEHLAVYCONDSHP 237
QY 229 YTFGGGTMLEIK 240
DB 238 LTFGAGTLEIK 249

RESULT 9

Q6S2Q7 PRELIMINARY; PRT; 248 AA.
AC Q6S2Q7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pal L.H., FitzGerald D.J., Williamson M., Pastan I.,
RT "B3 (Fv)-PE38DEL, a single-chain immunotoxin that causes complete
regression of a human carcinoma in mice."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
DR EMBL; S57990; AAB19971.2; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00406; IG_V; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 46.9%; Score 590; DB 2; Length 248;
Best Local Similarity 48.2%; Pred. No. 3.8e-39;
Matches 120; Conservative 45; Mismatches 72; Indels 12; Gaps 4;

QY 1 EIQLVSGPELKKPGETVTKISCKASGYTPANYGMNMMKQAPGKGLKMGWINTYTGSTY 60
DB 2 DVKLVESGGGLVPGGSLKISCKASGYTFTDTHAIHMAKQPEQGLMIGVTSFGNDIKY 61
QY 61 ADDPKERFAFSLTETSAITTAHLQINNLRNEDSATYFCARRFPAYWGQGLTVSVAS 116

DB 62 SDTVKGRFTISRDNANRLTYLQMSRLKSEDTAIVSCARGLAWGAFWYVQGTLYTVS-- 119

QY 117 ISSSSGGSSSSSSSSSDIQMTQSPSSLSALGERVSLTCRASODI-----GMS-LTWLQO 171

DB 120 -GGGGGGGGGGGGGGSDVLTMTQSPVLSLGDQASISCRSSQIIVHNGNVTYEMWYIQ 178

QY 172 EDDGTIKRLIYVTSLSLSDSGRSGRSGSDYSLTISLSSEDFVYVYVCLQVAIPPYTE 231

DB 179 KCGQSPKLLIYVSNRFGSEVPDRFSSGSGTDTLTKISRVHADLGVYVCPGSHVPTTF 238

QY 232 GGGTNLEIK 240

DB 239 GSGTKLEIK 247

RESULT 10

ID 099LA6 PRELIMINARY; PRT; 484 AA.

AC 099LA6; 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxId=10090;

RA STRAIN=mix FVB/N; TISSUE=Mammary tumor; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603399;

RA Straube R.L., Feltgoid E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Scheifer C.F., Bhat N.K., Hopfner R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diacchion M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., White J., Helton E., Ketterman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield J.E., Krzywinski M.T., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RP SEQUENCE FROM N.A.

RA STRAIN=mix FVB/N; TISSUE=Mammary tumor; Straube R.; Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DB EMBL; BC003495; AA03495.1; -.

DR PIR; F33932; F33932.

DR PIR; S19663; S19663.

DR HSSP; P01810; 2F8J.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_C1.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF07654; C1-sec; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.

KW Hypothetical protein.

SEQUENCE 484 AA; 52567 MW; 8EAEAF9BCF582FA CRC64;

Matches 123; Conservative 32; Mismatches 52; Indels 122; Gaps 9;

QY 1 EIQLYVSGPELKKPGETVVISCKASGYTPANTGAMMKAPKGLKMGHINTYTGQSTY 60

DB 20 QIQLVSGPELKKPGETVVISCKASGYTPDMSMHVKKAPGKGLMGKMGVNIETESVY 79

QY 61 ADDPFRFAFSLTETSATTHLQINNLRNEDSAITYFCAR-----FGFAVWGQGTLYSVS 114

DB 80 ADDPFRFAFSLTETSATTHLQINNLKNDTATYFCARSDYDIYDIAMVWGQGTLYSVS 139

QY 115 A-----SISS-----SGSSSSSSSSSGSDIQMTQSPSSLSA 146

DB 140 SESARNPTIYPLTPPALSSDPVITGLIDYFPGSGTMVTVWCKSGKIDITTVFPALAS 199

QY 147 S----- 147

DB 200 GGRYTWSSQTLTFAVECPGESEVKCSVOHDSNPVDELVNCSGPPTPTTSCOPSLS 259

QY 148 -----LGERVSLTCRAS---QDIGNSLTWLQOEP-----DGTIKRLI-----YAT 184

DB 260 LQRPALIEDLLSGSDASITTLNGLNRPBGAVFTW---EFTGKDAVQKAVQNSCGCYISV 316

QY 185 SSLDSGVPRFSGRSGSDYSLTISLES 213

DB 317 SSVLPQCAERMN---SGASFCTVTHPES 342

RESULT 11

ID KVSQ MOUSE STANDARD; PRT; 130 AA.

AC P01639; P01640; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region MOPC 41 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxId=10090;

RA STRAIN=FROM N.A.

RP MEDLINE=79221900; PubMed=111146;

RX Seidman J.G., Max E.B., Leder P.; "A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.";

RT Nature 280:370-375(1979).

RL [2]

RP SEQUENCE OF 1-33.

RA Buretein Y., Schechter I.; "Amino acid sequence of the NH2-terminal extra piece segments of the RT precursors of mouse immunoglobulin lambda1-type and kappa-type light chains.";

RT Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).

RL [3]

RP SEQUENCE OF 23-130.

RX MEDLINE=67056897; PubMed=4162931;

RA Gray W.R., Dreyer W.J., Hood L.; "Mechanism of antibody synthesis: size differences between mouse kappa chains.";

RT Science 155:465-467(1967).

CC -I- MISCELLANEOUS: This precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polybomes.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A33211; KVM5M4.

DR HSSP; P01594; 1JVS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region; Signal.

```
FT SIGNAL 1 22
FT CHAIN 23 130 Ig kappa chain V-V region MOPC 41.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 128 Framework-4.
FT DISULFID 45 110 By similarity.
FT VARIANT 1 2 Missing (in 25% of the molecules).
FT NON_TER 130
SQ SEQUENCE 130 AA; 14311 MW; 5E9FE71D5F1BEC CRC64;

Query Match 40.4%; Score 508; DB 1; Length 130;
Best Local Similarity 93.5%; Pred. No. 6e-33;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 134 DIQMTQSPSSLSASLGERSVLTCSRASQDIGNSLTWLQEPDGTIKRLIYATSSLDGVPK 193
Db 23 DIQMTQSPSSLSASLGERSVLTCSRASQDIGNSLTWLQEPDGTIKRLIYATSSLDGVPK 82

Qy 194 RFGSGRSGSDYSLTITSSLESDPVDYVYCYLQYAFPTFGGNTLEIKR 241
Db 83 RFGSGRSGSDYSLTITSSLESDPVDYVYCYLQYASPTFGGNTLEIKR 130

RESULT 12
Q925S9 PRELIMINARY; PRT; 127 AA.
ID 0925S9;
AC 0925S9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF.";
RL Hydridoma 18:193-202(1999).
DR EMBL; AF124721; AK55120.1; -.
DR HSSP; P01594; 1UV5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BBB8981FAS CRC64;

Query Match 39.1%; Score 492; DB 2; Length 127;
Best Local Similarity 91.6%; Pred. No. 1.1e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 134 DIQMTQSPSSLSASLGERSVLTCSRASQDIGNSLTWLQEPDGTIKRLIYATSSLDGVPK 193
Db 21 DIQMTQSPSSLSASLGERSVLTCSRASQDIGNSLTWLQEPDGTIKRLIYATSSLDGVPK 80

Qy 194 RFGSGRSGSDYSLTITSSLESDPVDYVYCYLQYAFPTFGGNTLEIKR 240
Db 81 RFGSGRSGSDYSLTITSSLESDPVDYVYCYLQYASPTFGGNTLEIKR 127

RESULT 13
Q683Y7 PRELIMINARY; PRT; 116 AA.
ID 0683Y7;
AC 0683Y7;
```

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Phalipon A., Costachel C., Thunizat A., Nato F.;
RT "Anti-11polysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784033; CAH04483.1; -.
DR InterPro; IPR003599; IG_.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12863 MW; 5EC11AD02B911952 CRC64;

Query Match 37.4%; Score 470.5; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 5.2e-30;
Matches 87; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EIQVQSGPELKKPEETIKSCKASGYTPFANYGMNMQAEGKIKMGMINTTYGQSTY 60
Db 1 EIVQLQSGSPOLKTPPEETIEICKASVYVTLTDYSLHWVQGGKGLRMWGMINTETGEPA 60

Qy 61 ADDFERAFPSLETATTAHIOINNLRNEDSATYFCA-RRPGFAYWGGTLVSVSA 115
Db 61 ADDFERAFPSLETATTAHIOINNLKNEDTRATYFCAGIRYDGAIVGGTLVYSA 116

RESULT 14
Q65ZL3 PRELIMINARY; PRT; 140 AA.
ID 065ZL3;
AC 065ZL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tg10H (Fragment).
GN Name=Tg10H;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96269537; PubMed=8669031; DOI=10.1016/0022-1759(96)00043-9;
RA Noel D., Bernard T., Navarro-Teuion I., Marin M., Martineto J.P.,
RA Ducancel F., Mani J.C., Pau B., Plechaczky M., Biard-Plechaczky M.;
RT "Analysis of the individual contributions of immunoglobulin heavy and
RT light chains to the binding of antigen using cell transfection and
RT plasmom resonance analysis.";
RL J. Immunol. Methods 193:177-187(1996).
DR EMBL; S82492; AAB37434.2; -.
DR InterPro; IPR003599; IG_.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965FA3 CRC64;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:19:49 ; Search time 29.9521 seconds
(without alignments)
193.690 Million cell updates/sec

Title: US-09-887-853-8
Perfect score: 66
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16dec04:*
1: geneeqp19808:*
2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20038:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 66 | 100.0 | 15 | 2 | AAR39572 |
| 2 | 66 | 100.0 | 15 | 3 | AA90828 |
| 3 | 66 | 100.0 | 15 | 4 | AAU08688 |
| 4 | 66 | 100.0 | 15 | 4 | AAU04949 |
| 5 | 66 | 100.0 | 15 | 7 | ABW00718 |
| 6 | 66 | 100.0 | 15 | 8 | ADN60232 |
| 7 | 66 | 100.0 | 15 | 8 | ADR38601 |
| 8 | 66 | 100.0 | 17 | 3 | AA67939 |
| 9 | 66 | 100.0 | 17 | 3 | AAO17004 |
| 10 | 66 | 100.0 | 17 | 6 | ADB24918 |
| 11 | 66 | 100.0 | 17 | 7 | ADB24915 |
| 12 | 66 | 100.0 | 17 | 7 | ABU10017 |
| 13 | 66 | 100.0 | 17 | 8 | ADQ28276 |
| 14 | 66 | 100.0 | 31 | 3 | AA15670 |
| 15 | 66 | 100.0 | 31 | 5 | AAO22543 |
| 16 | 66 | 100.0 | 31 | 5 | ABP97039 |
| 17 | 66 | 100.0 | 31 | 8 | ADN60233 |
| 18 | 66 | 100.0 | 34 | 5 | ABP56042 |
| 19 | 66 | 100.0 | 243 | 2 | AAW02280 |
| 20 | 66 | 100.0 | 243 | 2 | AAW53170 |
| 21 | 66 | 100.0 | 243 | 2 | AAW80424 |
| 22 | 66 | 100.0 | 243 | 7 | ABW00716 |
| 23 | 66 | 100.0 | 246 | 2 | AAAR39569 |
| 24 | 66 | 100.0 | 261 | 2 | AAAR44230 |
| 25 | 66 | 100.0 | 433 | 2 | AAAR91073 |

| | | | | | | |
|----|----|-------|-----|---|-----------|----------------------|
| 26 | 66 | 100.0 | 433 | 2 | AAW07598 | AAW07598 Basic fib |
| 27 | 66 | 100.0 | 433 | 3 | AA90459 | AA90459 bGCF/ser |
| 28 | 66 | 100.0 | 433 | 7 | ADC34725 | ADC34725 Human DRG |
| 29 | 66 | 100.0 | 433 | 7 | ADH92143 | ADH92143 Fibroblasts |
| 30 | 62 | 93.9 | 246 | 2 | AAAR27245 | AAAR27245 Light (VL |
| 31 | 62 | 93.9 | 246 | 2 | AAAR44229 | AAAR44229 Chimeric |
| 32 | 62 | 93.9 | 252 | 2 | AAW02279 | AAW02279 26-10 ant |
| 33 | 62 | 93.9 | 252 | 2 | AAW53169 | AAW53169 26-10 ant |
| 34 | 62 | 93.9 | 252 | 2 | AAW80423 | AAW80423 Anti-digo |
| 35 | 62 | 93.9 | 252 | 7 | ABW00715 | ABW00715 26-10 bFv |
| 36 | 62 | 93.9 | 367 | 2 | AAAR27244 | AAAR27244 Sequence |
| 37 | 62 | 93.9 | 471 | 2 | AAAR27246 | AAAR27246 Sequence |
| 38 | 60 | 90.9 | 15 | 5 | AAAG80185 | AAAG80185 Fusion co |
| 39 | 60 | 90.9 | 15 | 6 | ABU08677 | ABU08677 Human bin |
| 40 | 60 | 90.9 | 250 | 2 | AAW02278 | AAW02278 7A1F8 ant |
| 41 | 60 | 90.9 | 250 | 2 | AAW29261 | AAW29261 Anti-C-er |
| 42 | 60 | 90.9 | 250 | 2 | AAW22400 | AAW22400 Single ch |
| 43 | 60 | 90.9 | 250 | 2 | AAW47012 | AAW47012 Single ch |
| 44 | 60 | 90.9 | 250 | 2 | AAW53168 | AAW53168 7A1F8 ant |
| 45 | 60 | 90.9 | 250 | 2 | AAW80422 | AAW80422 Anti-C-er |

ALIGNMENTS

RESULT 1
AAR39572
ID AAR39572 standard; protein; 15 AA.
XX
AC AAR39572;
XX
DT 25-MAR-2003 (revised)
DT 07-FEB-1994 (first entry)
XX
DE Sequence of a new linker.
XX
KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW biosynthetic single polypeptide chain binding site.
XX
OS Synthetic.
XX
PN WO9316185-A2.
XX
PD 19-AUG-1993.
XX
PF 05-FEB-1993; 93WO-US001055.
XX
PR 06-FEB-1992; 92US-00831967.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (CETU) CETUS ONCOLOGY CORP.
XX
PI Huston JS, Huston LL, Ring DB, Oppermann H;
XX WPI. 1993-272889/34.
XX DR N-PSDB; AAQ46087.
XX
PT New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT imaging or treating breast or ovarian cancer etc.
XX
PS Example; Page 70; 87pp; English.
XX
XX c-erbB-2 refers to a protein antigen expressed on the surface of tumour
XX cells, such as breast and ovarian tumour cells, which is an approx.
XX 200,000 mol. wt. acidic glycoprotein having an isoelectric pt. of about
XX 5.3 (see AAQ46083, AAR39568). A single chain Fv (bFv) is a covalently
XX linked VH-VL heterodimer which is expressed from a gene fusion including
XX VH- and VL- encoding genes connected by a peptide-encoding linker. Such
XX linker sequences are set forth in AA residues 116-135 in AAR39569, which
XX includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084
XX produced having a binding affinity for a c-erbB-2 related antigen.
XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 15 AA;
SQ

Query Match 100.0%; Score 66; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15
Db 1 SSSSSSSSSSSSSG 15

RESULT 2
AA90828
ID AA90828 standard; peptide; 15 AA.

XX
AC AA90828;

XX 29-AUG-2000 (first entry)

XX Linker amino acid sequence SEQ ID NO:31.

XX Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW antibody; tumour; human; mucin; cancer; cytosolic; hybridoma;
KW specific binding assay; affinity purification; drug targeting;
KM toxin targeting; imaging; genetic; therapeutic.

XX Synthetic.

XX US6054561-A.

XX 25-APR-2000.

XX 07-JUN-1995; 95US-00483749.

XX 08-FEB-1984; 84US-00577976.

XX 11-JAN-1985; 85US-00690750.

XX 21-MAR-1986; 86US-00842476.

XX 08-MAY-1988; 88US-00190778.

XX 11-AUG-1994; 94US-00288981.

XX (CHIR) CHIRON CORP.

XX Ring DB;

XX WPI; 2000-338508/29.

XX Monoclonal antibody capable of binding to human breast cancer antigen

XX useful for affinity purification, drug or toxin targeting, imaging, and

XX treating cancer.

XX Disclosure; Col 77; 57pp; English.

XX The present invention describes a monoclonal antibody (Mab) (I) that

XX binds to a human breast cancer antigen that is also bound by Mab 454C11

XX and 520C9 (produced hybridoma ATCC HB9484 and HB8696, respectively). Also

XX described is a hybridoma that produces (I). (I) is useful in specific

XX binding assays, affinity purification, drug or toxin targeting, imaging,

XX and genetic or immunological therapeutics for various cancers. The

XX present sequence represents a linker amino acid sequence which is used in

XX the exemplification of the present invention

XX Sequence 15 AA;

XX Query Match 100.0%; Score 66; DB 3; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.012;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15
Db 1 SSSSSSSSSSSSSG 15

RESULT 3
AAU08688
ID AAU08688 standard; peptide; 15 AA.

XX
AC AAU08688;

XX 18-DEC-2001 (first entry)

XX Antibody L19-Fibronectin-2 (IL-2) fusion protein amino acid linker.

XX Angiogenesis; extracellular matrix; ED-B domain; fibronectin; lesion;

XX IL-2; doxorubicin; interleukin-12; interferon-gamma; IL-12; IFN-gamma;

XX Tumour Necrosis Factor alpha; TNF alpha; tissue factor protein; angiotensin;

XX electrochemical potential; tumour; cancer; rheumatoid arthritis;

XX diabetic retinopathy; age related muscular degeneration; cytosolic;

XX antirheumatic; antiarthritic; antidiabetic; ophthalmological.

XX Synthetic.

XX WO200162298-A2.

XX 30-AUG-2001.

XX 22-FEB-2001; 2001WO-IB000382.

XX 24-FEB-2000; 2000US-0184767P.

XX 21-DEC-2000; 2000US-0257192P.

XX (PHIL-) PHILGEN SRL.

XX Zardi L, Neri D, Carmemola B, Nilsson F, Tarli L, Borsi L;

XX Halin C;

XX WPI; 2001-596713/67.

XX Novel conjugate for treating lesions, comprises a specific binding member

XX specific for extra-cellular matrix component present in lesions, and a

XX molecule that exerts biocidal/cytotoxic effect on target cells in

XX lesions.

XX Example 1; Page 30; 89pp; English.

XX The invention relates to a conjugate comprising a molecule that exerts a

XX biocidal or cytotoxic effect on target cells in lesions of pathological

XX angiogenesis and an antibody (L19) directed against an extracellular

XX matrix component (the ED-B domain of fibronectin) which is present in the

XX lesions. Examples of biocidal or cytotoxic molecules include fibronectin-

XX 2 (IL-2), doxorubicin, interleukin-12 (IL-12), interferon-gamma (IFN-

XX gamma), Tumour Necrosis Factor alpha (TNF alpha) tissue factor protein.

XX These proteins may interact with a membrane-bound receptor on the target

XX cell or perturb the electrochemical potential of the cell membrane. The

XX treatable disorders include tumours, rheumatoid arthritis, diabetic

XX retinopathy, age related muscular degeneration and angiotensin. This

XX sequence represents an amino acid linker encoded by a PCR primer used in

XX the construction of an L19-IL-2 fusion protein

XX Sequence 15 AA;

XX Query Match 100.0%; Score 66; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 0.012;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSSSSSSSSSSSSG 15
Db 1 SSSSSSSSSSSSSG 15

RESULT 4
AAU04949
ID AAU04949 standard; peptide; 15 AA.

XX
AC AAU04949;

XX

DT 24-OCT-2001 (first entry)
XX
XX Humanised anti-p185 antibody/IL-2 fusion protein, linker peptide #2.
DE
XX Humanised; antibody; p185; 520C9H; interleukin-2; IL-2; immunoconjugate;
KW cancer; tumour; adenocarcinoma; fusion protein.
XX
XX Synthetic.
XX WO200153354-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US0001919.
XX
XX 20-JAN-2000; 2000US-0177258P.
XX
XX (CHIR) CHIRON CORP.
XX (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
XX (HAMI-) HAMILTON REGIONAL CANCER CENT.
XX
XX Auctin R, Kwok CS, Ring DB;
XX
XX WPI; 2001-451904/48.
XX
XX Novel immunoconjugate useful for inhibiting tumor cell growth in vivo
PT comprises a humanized anti-p185 antibody linked to an interleukin-2
PT polypeptide.
XX
XX PS Disclosure; Page 16; 74pp; English.
XX
XX The sequence represents a linker peptide used to make a humanised anti-
CC p185 (520C9) single chain antibody/human interleukin-2 (IL-2) fusion
CC protein. The fusion protein (or immunoconjugate) is used to inhibit the
CC growth of tumours or cancers particularly those characterized by
CC overexpression of p185 e.g. human adenocarcinomas and malignant and/or
CC benign tumours of the breast, renal system, salivary gland,
CC gastrointestinal tract or gastric tumours
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 100.0%; Score 66; DB 4; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.012;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSSSGSSSSSGSSSG 15
XX |||||||||
XX DB 1 SSSSGSSSSSGSSSG 15
XX
XX RESULT 5
XX ABW00718
XX ID ABW00718 standard; peptide; 15 AA.
XX
XX AC ABW00718;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Linker #2, peptide used in the invention.
XX
XX KW Cell proliferation; cytotoxic agent; drug targeting.
XX
XX OS Unidentified.
XX
XX PN US2002168375-A1.
XX
XX PD 14-NOV-2002.
XX
XX PF 21-JUN-2001; 2001US-00887853.
XX
XX PR 06-FEB-1992; 92US-00831967.
XX PR 07-OCT-1993; 93US-00133804.
XX PR 05-JUN-1995; 95US-00462641.
XX

PR 26-APR-2000; 2000US-00558741.
XX
XX (CHIR) CHIRON CORP.
XX
XX PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
XX DR WPI; 2003-765156/72.
XX
XX PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
XX PS Disclosure; Page 2; 30pp; English.
XX
XX The invention relates to a binding protein formulation for targeting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targeting drugs that inhibit cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is a linker peptide used in the invention
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 100.0%; Score 66; DB 7; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.012;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SSSSGSSSSSGSSSG 15
XX |||||||||
XX DB 1 SSSSGSSSSSGSSSG 15
XX
XX RESULT 6
XX ADN60232
XX ID ADN60232 standard; protein; 15 AA.
XX
XX AC ADN60232;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Linker peptide.
XX
XX KW linker; self-assembled monolayer.
XX
XX OS Synthetic.
XX
XX PN US6723517-B1.
XX
XX PD 20-APR-2004.
XX
XX PF 02-JUN-1999; 99US-00324258.
XX
XX PR 02-JUN-1998; 98US-0087766P.
XX
XX PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
XX
XX PI Bamdad CC;
XX
XX DR WPI; 2004-386879/36.
XX
XX PT Determining of distance between binding sites on target molecule
PT comprises contacting target molecule with self-assembled monolayer, and
PT identifying controlled geometry with lowest density.
XX
XX PS Disclosure; SEQ ID NO 18; 37pp; English.
XX
XX The invention relates to a method for determination of distance between
CC binding sites on a target molecule, involving contacting the target
CC molecule with a self-assembled monolayer comprising binding moieties
CC immobilised with respect to each other in controlled geometries,
CC identifying the controlled geometry with lowest density of immobilised

CC binding moieties that elicits a jump in affinity for the target molecule,
 CC and determining the distance between immobilised binding moieties in the
 CC controlled geometry with the lowest density to determine the distance
 CC between binding sites on the target molecule. The self-assembled
 CC monolayers incorporate thiol species capable of displaying a binding
 CC moiety to the target molecule, and inert spacer thiol component. Changes
 CC in binding affinity are correlated to a density of the thiol species.
 CC Statistical calculations are applied to a critical binding moiety density
 CC and thiol packing dimensions to determine a probable distance between the
 CC immobilised binding moieties. Extracted surface information is used in
 CC rational design of multi-valent drugs. Surface plasmon resonance is used
 CC to measure binding affinities between immobilized binding moieties and
 CC target molecule in solution. The target molecule is a protein complex.
 CC The thio species is a nitrilo tri-acetic acid terminated thiol. The
 CC present sequence represents a linker peptide which was used with
 CC immobilised binding moieties in the method of the invention.

XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 66; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 0.012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSG 15
 |||||
 Db 1 SSSSGSSSSSSSG 15

RESULT 7
 ADR38601
 ID ADR38601 standard; peptide; 15 AA.
 XX ADR38601;
 AC
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Anti-botulinum neurotoxin antibody associated linker #3.
 DE
 XX
 XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; linker.
 XX
 XX Synthetic.
 OS
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNITV CALIFORNIA.
 XX
 PI Marks JD, Amersdorfer P;
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 PS Disclosure; SEQ ID NO 3; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (i) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1G6, 3D12, B4, 1F3, hUC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surpluses. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a linker associated with the anti-BoNT/A-antibodies of the
 CC invention. Note: This sequence is found in the sequence listing but is
 CC not further described in the specification.

XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 66; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 0.012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSSSSG 15
 |||||
 Db 1 SSSSGSSSSSSSG 15

RESULT 8
 AAY67939
 ID AAY67939 standard; peptide; 17 AA.
 XX AAY67939;
 AC
 XX
 DT 27-MAR-2000 (first entry)
 XX
 XX EPOa-hSA fusion protein peptide linker #2.
 DE
 XX
 XX Erythropoietin analogue human serum albumin fusion protein; infection;
 KM EPOa-hSA fusion protein; peptide linker; HIV; cytostatic; antianemic;
 KM anaemia; renal failure; blood loss; cancer; nutraceutical; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 PN WO9966054-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 15-JUN-1999; 99WO-US013438.
 XX
 PR 15-JUN-1998; 98US-0089343P.
 XX
 PA (GENZ) GENZYME TRANSGENICS CORP.
 XX
 PI Young MW, Meade HM, Krane IW;
 XX
 DR WPI; 2000-097749/08.
 XX
 PT An erythropoietin analog-human serum albumin fusion protein, used for,
 PT e.g. treatment of HIV infection.
 XX
 PS Claim 19; Page 53; 61pp; English.
 XX
 CC The present invention describes erythropoietin analogue-human serum
 CC albumin (EPOa-hSA) fusion proteins having at least one amino acid residue
 CC of the EPOa moiety altered such that a site, which serves as a site for
 CC glycosylation in EPO does not serve same purpose in the EPOa. The present
 CC sequence represents a specifically claimed peptide linker for use in the
 CC construction of an EPOa-hSA fusion protein. The EPOa-hSA fusion protein

CC can be used in treatment of a subject in need of EPO, e.g. for a patient
CC suffering from anemia associated with renal failure, chronic disease,
CC HIV infection, blood loss or cancer. The EPOa-hsa fusion protein can be
CC included in a nutraceutical, such as an infant feeding formula. The EPOa-
CC hsa constructs can be used as part of a gene therapy protocol to deliver
CC nucleic acids encoding an EPOa-hsa fusion protein
XX

XX Sequence 17 AA;

Query Match 100.0%; Score 66; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSGSSSG 15
Db 1 SSSSGSSSGSSSG 15

RESULT 9

AA017004 standard; peptide; 17 AA.

AA017004;

29-MAY-2002 (first entry)

Linker peptide used to construct alpha-MSH concatamer SEQ ID NO: 68.

Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
immunosuppressive; antineoplastic; antirheumatic; antiarthritic;
antischismatic; antibacterial; dermatological; antipsoriatic;
antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
diabetes; uveitis; coeliac disease; linker.

Synthetic.

WO200206316-A2.

24-JAN-2002.

16-JUL-2001; 2001WO-US022263.

14-JUL-2000; 2000US-0218381P.

18-AUG-2000; 2000US-0226382P.

06-OCT-2000; 2000US-0238380P.

29-DEC-2000; 2000US-0258764P.

14-JUN-2001; 2001US-0298317P.

(ZYCO-) ZYCO INC.

Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;

WPI, 2002-195801/25.

Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
stimulating hormone concatamer or its analog, for treating inflammatory
or autoimmune disorders.

Disclosure; Page 16; 89pp; English.

The present invention relates to a nucleic acid comprising a sequence
encoding a fusion polypeptide having an alpha-melanocyte stimulating
hormone (MSH) concatamer. The sequences are useful for treating an
individual suffering from, or at risk of, a disorder of the immune system
e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
present sequence is a linker peptide described in the exemplification of
the invention

SQ Sequence 17 AA;

Query Match 100.0%; Score 66; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSGSSSG 15
Db 1 SSSSGSSSGSSSG 15

RESULT 10

ADB24918 standard; peptide; 17 AA.

ADB24918;

20-NOV-2003 (first entry)

Peptide linker #4.

antibody generation; rapid protein production;
efficient protein production; linker.

Synthetic.

US2003049801-A1.

13-MAR-2003.

14-FEB-2002; 2002US-00077210.

10-SEP-2001; 2001US-0318474P.

(WUCC/) WU C.

(LINR/) LIN R.

(HSUP/) HSU P.

Wu C, Lin R, Hsu P;

WPI, 2003-605754/57.

Generating an antibody for basic research and therapeutic purposes,
comprises producing a fusion protein in a first mammal and administering
the formed protein to a second mammal to generate an antibody against the
protein.

Disclosure; Page 3; 9pp; English.

The invention relates to a method of generating an antibody. The method
is useful in generating antibodies that may be used for basic research
and in the diagnosis and treatment of various diseases. The antibodies
may allow for the precise identification and quantitation of a particular
species of protein in a biological sample. The antibody may also be used
to modulate the activity or function of a protein which is useful for
treating a disease characterised by excessive or insufficient activity of
the protein. The method allows for the rapid and efficient production and
isolation of large amounts of protein or its portion in its native
conformation. The method avoids the time-consuming, expensive and
laborious tasks associated with the in vitro production and purification
of proteins. The present sequence represents a peptide linker.

Sequence 17 AA;

Query Match 100.0%; Score 66; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSGSSSG 15
Db 1 SSSSGSSSGSSSG 15

RESULT 11
ADB24915
ID ADB24915 standard; peptide; 17 AA.
XX
AC ADB24915;
XX
DT 20-NOV-2003 (first entry)
XX
DE Peptide linker #4.
XX
KM fusion protein purification; rapid protein production;
KW efficient protein production; high-throughput screening; linker.
XX
OS Synthetic.
XX
PN US2003049694-A1.
XX
PD 13-MAR-2003.
XX
PF 14-FEB-2002; 2002US-00077213.
XX
PR 10-SEP-2001; 2001US-0318474P.
XX
PA (WUCC/) WU C.
PA (LINR/) LIN R.
PA (HSUP/) HSU P.
XX
PI Wu C, Lin R, Hsu P;
XX
DR WPI; 2003-615799/58.
XX
PT Preparing purified fusion proteins useful to screen for target binding
PT molecule, by administering nucleic acid encoding the fusion protein to a
PT mammal, and isolating the fusion protein by removing a biological sample
PT from mammal.
XX
PS Disclosure; Page 3; 9pp; English.
XX
CC The invention relates to a method of preparing a purified fusion protein.
CC The method is useful for preparing fusion proteins. The method allows for
CC rapid and efficient, production and isolation of a protein encoded by any
CC nucleic acid sequence of interest. The method permits the high-throughput
CC screening of antibodies or other ligands directed against any protein
CC sequence, without the need to synthesise the protein sequence in vitro.
CC The method avoids the time-consuming, expensive and laborious tasks
CC associated with the in vitro production and purification of proteins. The
CC method avoids several of the difficulties associated with recombination
CC protein production in bacteria. The present sequence represents a peptide
CC linker.
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 66; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSSSSSSSSSSSSSG 15
Db 1 SSSSSSSSSSSSSSG 15
XX
RESULT 12
ABU10017
ID ABU10017 standard; peptide; 17 AA.
XX
AC ABU10017;
XX
DT 31-JUL-2003 (first entry)
XX
DE Alpha-MSH concatamer related linker peptide #5.
XX
KW Bladder disorder; cytoskeletal; antiinflammatory; immune response;
KW un-methylated CpG sequence; alpha-MSH; melanocortin receptor;
XX

KW bladder cancer; tumour; interstitial cystitis; inflammation; alpha-MSH;
KW melanocyte stimulating hormone.
XX
OS Unidentified.
XX
PN US2002193332-A1.
XX
PD 19-DEC-2002.
XX
PF 12-FEB-2002; 2002US-00074956.
XX
PR 12-FEB-2001; 2001US-0268175P.
XX
PA (HEDL/) HEDLEY M L.
XX
PI Hedley ML;
XX
DR WPI; 2003-447327/42.
XX
PT Modulating immune responses in a mammal with a bladder disorder e.g.
PT bladder cancer, by administering nucleic acids comprising un-methylated
PT CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to
PT the mammal.
XX
PS Disclosure; Page 5; 17pp; English.
XX
CC The invention describes a method of modulating an immune response in a
CC mammal, comprising identifying a mammal that has or is at risk for having
CC a bladder disorder, and administering: (a) an isolated nucleic acid (N1)
CC comprising an un-methylated CpG sequence to the mammal; (b) an isolated
CC nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal;
CC or (c) a peptide that binds to a melanocortin receptor to the mammal. The
CC method is useful for modulating immune response in a mammal having a
CC bladder disorder, where administration of (N1) results in an amelioration
CC of one or more symptoms of the disorder. Preferably, the method is useful
CC for modulating immune response in a mammal having bladder cancer (where
CC administration of (N1) results in a decrease in tumour size or activity),
CC or for modulating immune response in a mammal having interstitial
CC cystitis (where administration of (N1) results in a modulation of the
CC immune response from Th2 response to a Th1 response). The method is also
CC useful for modulating immune response in a mammal having bladder disorder
CC that is characterised by inflammation which is associated with symptoms
CC of interstitial cystitis or associated with a disruption of the integrity
CC of the bladder lining. This is the amino acid sequence of a linker
CC peptide useful in the creation of melanocyte stimulating hormone (alpha-
CC MSH) concatamers used in the method of treating bladder disorders
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 66; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSSSSSSSSSSSSSG 15
Db 1 SSSSSSSSSSSSSSG 15
XX
RESULT 13
ADQ28276
ID ADQ28276 standard; peptide; 17 AA.
XX
AC ADQ28276;
XX
DT 09-SEP-2004 (first entry)
XX
DE Peptide linker #4.
XX
KW gene therapy; transgenic; fusion protein; colon cancer; breast cancer;
KW prostate cancer; ovarian cancer; endometrial cancer.
XX
OS Synthetic.
XX

PN US2004117863-A1.
 XX
 PD 17-JUN-2004.
 XX
 PF 27-JUN-2003; 2003US-00608710.
 XX
 PR 18-SEP-1998; 98US-0101083P.
 PR 17-SEP-1999; 99US-00398610.
 XX
 PA (EDGE/) EDGE M D.
 PA (POL/) POLLOCK D.
 PA (ECHE/) ECHELARD Y.
 PA (MEAD/) MEADE H M.
 PA (RYBA/) RYBAK S M.
 XX
 PI Edge MD, Pollock D, Echelard Y, Meade HM, Rybak SM;
 DR WPI; 2004-449486/42.
 XX
 PT Making a transgenic fusion protein using a transgenic animal having a
 PT transgene expressing the fusion protein, useful for the diagnosing,
 PT preventing or treating colon, breast, prostate, ovarian and endometrial
 PT cancers.
 XX
 PS Disclosure; SEQ ID NO 9; 32pp; English.
 XX
 CC The invention relates to a method of making a transgenic fusion protein
 CC comprising providing a transgenic animal which includes a transgene which
 CC provides for the expression of the fusion protein, allowing the transgene
 CC to be expressed, and recovering the fusion protein, from the milk of the
 CC transgenic animal. The methods and compositions of the present invention
 CC are useful for the diagnosis, prevention and/or treatment of colon,
 CC breast, prostate, ovarian and endometrial cancers. The present sequence
 CC represents the amino acid sequence of a peptide linker.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 66; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 SSSSSSSSSSSSSSG 15
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 AAB15670
 ID AAB15670 standard; peptide; 31 AA.
 XX
 AC AAB15670;
 XX
 DT 01-DEC-2000 (first entry)
 XX
 DE Alpha V beta 3 receptor-specific peptide.
 XX
 KW Alpha V beta 3 receptor; colloid-electrode binding; drug screening;
 KW colloid derivatization.
 XX
 OS Unidentified.
 XX
 PN WO200043783-A2.
 XX
 PD 27-JUL-2000.
 XX
 PF 21-JAN-2000; 2000WO-US001504.
 XX
 PR 23-JAN-1999; 99US-0116975P.
 PR 03-MAY-1999; 99US-0132289P.
 PR 07-MAY-1999; 99US-0133148P.
 PR 12-MAY-1999; 99US-0133772P.
 XX
 PT (MINE-) MINERVA BIOTECHNOLOGIES CORP.

XX
 PI Bamdad CC, Bamdad RS;
 XX
 DR WPI; 2000-514740/46.
 XX
 PT Interaction of colloid-immobilized species with species on non-colloidal
 PT structures, useful in assays for monitoring or detecting interactions
 PT between chemical or biological species, particularly for drug screening.
 XX
 PS Example 43; Page 35; 95pp; English.
 XX
 CC The present sequence is a peptide which was used in an example describing
 CC the electronic detection of cells grown on conducting surfaces that were
 CC not coated with collagen. Cells were incubated with colloids that
 CC displayed ferrocene moieties and the present peptide, which is specific
 CC for the alpha V beta 3 receptor on the cell surface. Cells grown on a
 CC 100% ethynylphenyl thiol SAM-coated electrode produced current peaks only
 CC if incubated with colloids bearing the ligand specific for the alpha V
 CC beta 3 receptor and not when incubated with colloids derivatised with an
 CC irrelevant peptide. This example was used to demonstrate a method for
 CC enabling colloids to bind to non-colloidal structures such as electrodes,
 CC beads or cells. The method is useful in assays for monitoring or
 CC detecting interactions between chemical or biological species,
 CC particularly for drug screening, screening for inhibitors or activators
 CC of enzymes, identifying unknown targets or known ligands, detection of
 CC protein-protein interactions, detection of protein-ligand interactions,
 CC and detection of ligand-receptor interactions
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 66; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SSSSSSSSSSSSSSG 15
 DB 7 SSSSSSSSSSSSSSG 21
 RESULT 15
 AA022543
 ID AA022543 standard; peptide; 31 AA.
 XX
 AC AA022543;
 XX
 DT 28-OCT-2002 (first entry)
 XX
 DE GRGDS-containing peptide.
 XX
 KW Cytostatic; antitumour; angiogenesis inhibitor; L-histidine; suramin;
 KW quiescent acid; D-cycloserine; invasive cancer; metastatic tumour;
 KW endostatin; nanoparticle-based; alpha-V-beta3-vitronectin interaction;
 KW vitronectin.
 XX
 OS Unidentified.
 XX
 PN WO200239999-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 15-NOV-2001; 2001WO-US046221.
 XX
 PR 15-NOV-2000; 2000US-0248865P.
 PR 22-MAR-2001; 2001US-0277922P.
 XX
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
 XX
 PI Bamdad RS, Bamdad CC;
 XX
 DR WPI; 2002-490116/52.
 XX
 PT Use of a composition comprising L-histidine, quiescent acid, D-
 PT cycloserine, and suramin or their analogs for the treatment of invasive

PT cancer and metastatic tumors.

XX
PS Example 2; Page 4; 27pp; English.

XX
CC The invention relates to the treatment of a human patient involving the
CC administering of a composition comprising an angiogenesis inhibitor
CC selected from L-histidine, quisqualic acid, D-cycloserine or suramin or
CC their analogues to the patient. The treatment is useful against invasive
CC cancer and metastatic tumours. The advantage of the treatment is that the
CC composition can be given at a maximum amount while avoiding detrimental
CC side effects. The method provides a molecular target of the known
CC angiogenesis inhibitor, endostatin, and provides a high throughput,
CC nanoparticle-based in vitro assay that rapidly identifies compounds, both
CC natural and synthetic that inhibit angiogenesis by mimicking the effect
CC of endostatin. The compounds are readily modified and optimised to
CC produce analogues that are more effective than the parent compound. This
CC sequence represents a GRGDS-containing peptide of the invention. The
CC GRGDS peptide mimics full-length vitronectin and inhibits angiogenesis by
CC interrupting the alpha-V-beta3-vitronectin interaction relating to the
CC invention

XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 66; DB 5; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15

DB 7 SSSSSSSSSSSSSSG 21

Search completed: April 4, 2005, 15:47:21
Job time : 30.9521 secs

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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:33:25 ; Search time 7.66773 Seconds

(without alignments)
146.032 Million cell updates/sec

Title: US-09-887-853-8

Perfect score: 66

Sequence: 1 SSSSSSSSSSSSSSSG 15

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 66 | 100.0 | 15 | 1 | US-08-133-804-8 | Sequence 8, Appl1 |
| 2 | 66 | 100.0 | 15 | 1 | US-08-461-838-8 | Sequence 8, Appl1 |
| 3 | 66 | 100.0 | 15 | 2 | US-08-461-386-8 | Sequence 8, Appl1 |
| 4 | 66 | 100.0 | 15 | 2 | US-08-356-786-12 | Sequence 12, Appl1 |
| 5 | 66 | 100.0 | 15 | 2 | US-08-665-202-3 | Sequence 3, Appl1 |
| 6 | 66 | 100.0 | 15 | 3 | US-08-483-749A-31 | Sequence 31, Appl1 |
| 7 | 66 | 100.0 | 15 | 4 | US-09-315-574-3 | Sequence 3, Appl1 |
| 8 | 66 | 100.0 | 15 | 4 | US-09-324-258-18 | Sequence 18, Appl1 |
| 9 | 66 | 100.0 | 17 | 4 | US-09-333-213-4 | Sequence 4, Appl1 |
| 10 | 66 | 100.0 | 17 | 4 | US-10-077-210-4 | Sequence 4, Appl1 |
| 11 | 66 | 100.0 | 31 | 4 | US-09-324-258-19 | Sequence 19, Appl1 |
| 12 | 66 | 100.0 | 100 | 4 | US-09-411-067C-5 | Sequence 5, Appl1 |
| 13 | 66 | 100.0 | 243 | 1 | US-08-133-804-6 | Sequence 6, Appl1 |
| 14 | 66 | 100.0 | 243 | 1 | US-08-461-838-6 | Sequence 6, Appl1 |
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| 16 | 66 | 100.0 | 243 | 2 | US-08-356-786-4 | Sequence 4, Appl1 |
| 17 | 62 | 93.9 | 246 | 1 | US-08-257-341-7 | Sequence 7, Appl1 |
| 18 | 62 | 93.9 | 252 | 1 | US-08-133-804-4 | Sequence 4, Appl1 |
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| 22 | 62 | 93.9 | 471 | 1 | US-08-257-341-9 | Sequence 9, Appl1 |
| 23 | 60 | 90.9 | 250 | 1 | US-08-133-804-2 | Sequence 2, Appl1 |
| 24 | 60 | 90.9 | 250 | 1 | US-08-461-184-8 | Sequence 8, Appl1 |
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| 26 | 60 | 90.9 | 250 | 1 | US-08-464-589-8 | Sequence 8, Appl1 |
| 27 | 60 | 90.9 | 250 | 1 | US-08-461-838-2 | Sequence 2, Appl1 |

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| 28 | 60 | 90.9 | 250 | 2 | US-08-461-386-2 | Sequence 2, Appl1 |
| 29 | 60 | 90.9 | 622 | 2 | US-08-356-786-16 | Sequence 16, Appl1 |
| 30 | 57 | 86.4 | 212 | 4 | US-09-270-767-41907 | Sequence 41907, A |
| 31 | 54 | 81.8 | 13 | 1 | US-08-257-341-1 | Sequence 1, Appl1 |
| 32 | 54 | 81.8 | 239 | 4 | US-09-248-796A-16550 | Sequence 16550, A |
| 33 | 54 | 81.8 | 408 | 4 | US-09-543-681A-6442 | Sequence 6442, Ap |
| 34 | 54 | 81.8 | 475 | 2 | US-08-861-464-14 | Sequence 14, Appl1 |
| 35 | 54 | 81.8 | 475 | 2 | US-08-396-001-14 | Sequence 14, Appl1 |
| 36 | 54 | 81.8 | 475 | 3 | US-09-323-433A-14 | Sequence 14, Appl1 |
| 37 | 54 | 81.8 | 475 | 4 | US-09-826-752-14 | Sequence 14, Appl1 |
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| 39 | 54 | 81.8 | 1481 | 3 | US-08-599-654-40 | Sequence 40, Appl1 |
| 40 | 54 | 81.8 | 1481 | 3 | US-08-944-868A-40 | Sequence 40, Appl1 |
| 41 | 54 | 81.8 | 1481 | 3 | US-08-944-423A-40 | Sequence 40, Appl1 |
| 42 | 54 | 81.8 | 1481 | 3 | US-08-944-436-40 | Sequence 40, Appl1 |
| 43 | 53 | 80.3 | 180 | 4 | US-09-248-796A-22352 | Sequence 22352, A |
| 44 | 53 | 80.3 | 250 | 4 | US-09-248-796A-22487 | Sequence 22487, A |
| 45 | 53 | 80.3 | 442 | 4 | US-09-248-796A-21400 | Sequence 21400, A |

ALIGNMENTS

RESULT 1
US-08-133-804-8
Sequence 8, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppertmann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Teesta, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..15
OTHER INFORMATION: /note= "LINKER 2"
US-08-133-804-8
Query Match 100.0%; Score 66; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

RESULT 2

US-08-461-838-8

; Sequence 8, Application US/08461838

; Patent No. 5753204

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,838

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.

; REGISTRATION NUMBER: 34,637

; REFERENCE/DOCKET NUMBER: 2054/22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-248-7477

; TELEFAX: 617-248-7100

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-838-8

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

RESULT 3

US-08-461-386-8

; Sequence 8, Application US/08461386

; Patent No. 5837846

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,386

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.

; REGISTRATION NUMBER: 34,637

; REFERENCE/DOCKET NUMBER: 2054/22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-248-7477

; TELEFAX: 617-248-7100

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..15

; OTHER INFORMATION: /note= "LINKER 2"

US-08-461-386-8

QY 1 SSSSSSSSSSSSSG 15

Db 1 SSSSSSSSSSSSSG 15

RESULT 4

US-08-356-786-12

; Sequence 12, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pletcher, Testa, Hurwitz, & Thibault

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-12

Query Match 100.0%; Score 66; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 1 SSSSGSSSSSSSSSG 15

RESULT 5
US-08-665-202-3
Sequence 3, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
TITLE OF INVENTION: Tumor Antigens
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-3

Query Match 100.0%; Score 66; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 1 SSSSGSSSSSSSSSG 15

RESULT 6
US-08-483-749A-31
Sequence 31, Application US/08483749A
Patent No. 6054561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
NUMBER OF SEQUENCES: 33
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508,008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-749A-31

Query Match 100.0%; Score 66; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 1 SSSSGSSSSSSSSSG 15

RESULT 7
US-09-315-574-3
Sequence 3, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141

```

CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-3

Query Match          100.0%; Score 66; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 8
US-09-324-258-18
; Sequence 18, Application US/09324258
; Patent No. 6723517
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia C.
; TITLE OF INVENTION: THE USE OF SELF-ASSEMBLED MONOLAYERS TO
; TITLE OF INVENTION: PROBE THE STRUCTURE OF A TARGET MOLECULE
; FILE REFERENCE: M1015/7004/TJO
; CURRENT APPLICATION NUMBER: US/09/324,258
; CURRENT FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: U.S. 60/087,766
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker
US-09-324-258-18
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Query Match          100.0%; Score 66; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 9
US-09-333-213-4
; Sequence 4, Application US/09333213
; Patent No. 6548653
; GENERAL INFORMATION:
; APPLICANT: Young, Michael
; APPLICANT: Meade, Harry
; APPLICANT: Krane, Ian
; TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
; FILE REFERENCE: 10275/041001
; CURRENT APPLICATION NUMBER: US/09/333,213
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated linker sequence
US-09-333-213-4

Query Match          100.0%; Score 66; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 10
US-10-077-210-4
; Sequence 4, Application US/10077210
; Patent No. 6800462
; GENERAL INFORMATION:
; APPLICANT: Wu, Chung-Hsiun
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Hsu, Pei-Ling
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT PROTEINS IN VIVO AND USE FOR GENERATING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-004001
; CURRENT APPLICATION NUMBER: US/10/077,210
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/318,474
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker sequence
US-10-077-210-4

Query Match          100.0%; Score 66; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15
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RESULT 11
US-09-324-258-19
; Sequence 19, Application US/09324258
; Patent No. 6723517
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia C.
; TITLE OF INVENTION: THE USE OF SELF-ASSEMBLED MONOLAYERS TO
; FILE REFERENCE: M1015/7004/TUO
; CURRENT FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: U.S. 60/087,766
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IX-Linker-1X
US-09-324-258-19

Query Match          100.0%; Score 66; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 9 SSSSGSSSSSSSSSG 23

RESULT 12
US-09-411-067C-5
; Sequence 5, Application US/09411067C
; Patent No. 6576610
; GENERAL INFORMATION:
; APPLICANT: NUVAS, LLC
; APPLICANT: HOUSTON, L.L.
; TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFIC
; FILE REFERENCE: NUVAS1140
; CURRENT APPLICATION NUMBER: US/09/411,067C
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Spacer element
; NAME/KEY: REPEAT
; LOCATION: (1)..(5)
; OTHER INFORMATION: Spacer peptide variation; sequence repeated "n" times, where n =
US-09-411-067C-5

Query Match          100.0%; Score 66; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 1 SSSSGSSSSSSSSSG 15

RESULT 13
US-08-133-804-6
; Sequence 6, Application US/08133804
; Patent No. 5534254
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; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Tesca, Hurwitz & Thibault/Parent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/133,804
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-804-6

Query Match          100.0%; Score 66; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSSGSSSSSSSSSG 15
Db 118 SSSSGSSSSSSSSSG 132

RESULT 14
US-08-461-838-6
; Sequence 6, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Tesca, Hurwitz & Thibault/Parent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-6

Query Match 100.0%; Score 66; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15
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Db 118 SSSSGSSSGSSSG 132

RESULT 15
US-08-461-386-6
Sequence 6, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-6

Query Match 100.0%; Score 66; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15
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Db 118 SSSSGSSSGSSSG 132

Search completed: April 4, 2005, 16:00:54
Job time: 8.66773 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:56:43 ; Search time 22.1406 Seconds
(without alignments)
224.651 Million cell updates/sec

Title: US-09-887-853-8

Perfect score: 66
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 66 | 100.0 | 15 | 9 | US-09-144-886-3 |
| 2 | 66 | 100.0 | 15 | 9 | US-09-887-853-8 |
| 3 | 66 | 100.0 | 15 | 15 | US-10-204-581-1 |
| 4 | 66 | 100.0 | 15 | 15 | US-10-632-706-3 |
| 5 | 66 | 100.0 | 15 | 17 | US-10-683-547-8 |
| 6 | 66 | 100.0 | 17 | 13 | US-10-081-400-4 |
| 7 | 66 | 100.0 | 17 | 13 | US-10-074-956-19 |
| 8 | 66 | 100.0 | 17 | 14 | US-10-077-213-4 |
| 9 | 66 | 100.0 | 17 | 14 | US-10-077-210-4 |
| 10 | 66 | 100.0 | 17 | 16 | US-10-608-710-9 |
| 11 | 66 | 100.0 | 17 | 16 | US-10-768-873-4 |
| 12 | 66 | 100.0 | 31 | 10 | US-09-996-069-12 |
| 13 | 66 | 100.0 | 31 | 13 | US-10-003-661-1 |

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|----|----|-------|------|----|----------------------|-------------------|
| 14 | 66 | 100.0 | 243 | 9 | US-09-887-853-6 | Sequence 6, Appl1 |
| 15 | 66 | 100.0 | 252 | 17 | US-10-683-547-6 | Sequence 6, Appl1 |
| 16 | 62 | 93.9 | 252 | 17 | US-09-887-853-4 | Sequence 4, Appl1 |
| 17 | 62 | 93.9 | 252 | 17 | US-10-683-547-4 | Sequence 4, Appl1 |
| 18 | 60 | 90.9 | 250 | 9 | US-09-887-853-2 | Sequence 2, Appl1 |
| 19 | 60 | 90.9 | 250 | 17 | US-10-683-547-2 | Sequence 2, Appl1 |
| 20 | 57 | 86.4 | 1249 | 15 | US-10-369-493-6099 | Sequence 6099, Ap |
| 21 | 56 | 84.8 | 123 | 15 | US-10-767-701-35941 | Sequence 35941, A |
| 22 | 55 | 83.3 | 563 | 16 | US-10-437-963-198539 | Sequence 198539, |
| 23 | 54 | 81.8 | 94 | 9 | US-09-764-864-1273 | Sequence 1273, Ap |
| 24 | 54 | 81.8 | 104 | 9 | US-09-764-864-1276 | Sequence 1276, Ap |
| 25 | 54 | 81.8 | 108 | 9 | US-09-764-864-817 | Sequence 817, App |
| 26 | 54 | 81.8 | 112 | 9 | US-09-764-864-812 | Sequence 812, App |
| 27 | 54 | 81.8 | 156 | 9 | US-09-925-301-1154 | Sequence 1154, Ap |
| 28 | 54 | 81.8 | 160 | 15 | US-10-424-589-175646 | Sequence 175646, |
| 29 | 54 | 81.8 | 179 | 16 | US-10-437-963-199226 | Sequence 199226, |
| 30 | 54 | 81.8 | 203 | 15 | US-10-264-237-1938 | Sequence 1938, Ap |
| 31 | 54 | 81.8 | 256 | 14 | US-10-156-761-11972 | Sequence 11972, A |
| 32 | 54 | 81.8 | 386 | 14 | US-10-050-704-100 | Sequence 100, App |
| 33 | 54 | 81.8 | 386 | 16 | US-10-798-512-100 | Sequence 100, App |
| 34 | 54 | 81.8 | 406 | 16 | US-10-451-467A-262 | Sequence 262, App |
| 35 | 54 | 81.8 | 448 | 15 | US-10-108-260A-2481 | Sequence 2481, Ap |
| 36 | 54 | 81.8 | 472 | 15 | US-10-258-951-73 | Sequence 73, Appl |
| 37 | 54 | 81.8 | 475 | 9 | US-09-826-752-14 | Sequence 14, Appl |
| 38 | 54 | 81.8 | 475 | 15 | US-10-369-493-12092 | Sequence 22092, A |
| 39 | 54 | 81.8 | 475 | 17 | US-10-912-434-14 | Sequence 14, Appl |
| 40 | 54 | 81.8 | 544 | 14 | US-10-032-585-7924 | Sequence 7924, Ap |
| 41 | 54 | 81.8 | 593 | 15 | US-10-258-951-72 | Sequence 72, Appl |
| 42 | 54 | 81.8 | 623 | 13 | US-10-108-605-125 | Sequence 125, App |
| 43 | 54 | 81.8 | 623 | 13 | US-10-108-605-129 | Sequence 129, App |
| 44 | 54 | 81.8 | 679 | 15 | US-10-282-122A-78228 | Sequence 78228, A |
| 45 | 54 | 81.8 | 946 | 10 | US-09-840-746-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-144-886-3
; Sequence 3, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144, 886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: [(Ser)4Gly]3
US-09-144-886-3
Query Match 100.0%; Score 66; DB 9; Length 15;
Best Local Similarity 100.0%; Pred.No. 0.062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSSSSSSSSSSSSSG 15
DB 1 SSSSSSSSSSSSSSG 15
RESULT 2
US-09-887-853-8
; Sequence 8, Application US/09887853
; Patent No. US20020168375A1

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; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; Oppermann, Hermann
; Houston, L. L.
; Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..15
; OTHER INFORMATION: /note="LINKER 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-887-853-8
;
; Query Match 100.0%; Score 66; DB 9; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 SSSSGSSSSSGSSSG 15
; Db 1 SSSSGSSSSSGSSSG 15
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; RESULT 3
; US-10-204-581-1
; Sequence 1, Application US/10204581
; Publication No. US20040013640A1
; GENERAL INFORMATION:
; APPLICANT: Zardi, Luciano
; APPLICANT: Neri, Dario
; APPLICANT: Carmemolla, Barbara
; APPLICANT: Nilsson, Fredrik
; APPLICANT: Tarli, Lorenzo
; APPLICANT: Borsi, Laura
; APPLICANT: Halli, Cornelia
; TITLE OF INVENTION: Compositions and methods for treatment of angiogenesis
; FILE REFERENCE: 0380-P02964US0
; CURRENT APPLICATION NUMBER: US/10/204,581
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; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/IB01/00382
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/184,767
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/257,192
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linker
; US-10-204-581-1
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; Query Match 100.0%; Score 66; DB 15; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 SSSSGSSSSSGSSSG 15
; Db 1 SSSSGSSSSSGSSSG 15
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; RESULT 4
; US-10-632-706-3
; Sequence 3, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: protein linker
; US-10-632-706-3
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; Query Match 100.0%; Score 66; DB 16; Length 15;
; Best Local Similarity 100.0%; Pred. No. 0.062;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SSSSGSSSSSGSSSG 15
; Db 1 SSSSGSSSSSGSSSG 15
;
; RESULT 5
; US-10-683-547-8
; Sequence 8, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
; APPLICANT: Huston, J.
; APPLICANT: Houston, L.L.
; APPLICANT: Ring, D.
; APPLICANT: Oppermann, H.
; TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
; FILE REFERENCE: CIBT-P01-130
; CURRENT APPLICATION NUMBER: US/10/683,547
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/ CURRENT FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: US/09/558,741
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: 07/831,967
/ PRIOR FILING DATE: 1992-02-06
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker 2
US-10-683-547-8

Query Match      100.0%; Score 66; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 6
US-10-081-400-4
/ Sequence 4, Application US/10081400
/ Publication No. US2002015598A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, Michael
/ APPLICANT: Meade, Harry
/ APPLICANT: Krane, Ian
/ TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
/ FILE REFERENCE: 10275/041001
/ CURRENT APPLICATION NUMBER: US/10/081,400
/ CURRENT FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 09/333,213
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated linker sequence
US-10-081-400-4

Query Match      100.0%; Score 66; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 7
US-10-074-956-19
/ Sequence 19, Application US/10074956
/ Publication No. US20020193332A1
/ GENERAL INFORMATION:
/ APPLICANT: Hedley, Mary Lynne
/ TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
/ FILE REFERENCE: 08191-022001
/ CURRENT APPLICATION NUMBER: US/10/074,956
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: 60/268,175
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 17
```

```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-074-956-19

Query Match      100.0%; Score 66; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 8
US-10-077-213-4
/ Sequence 4, Application US/10077213
/ Publication No. US20030049694A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Chung-Hsiun
/ APPLICANT: Lin, Rong-Hwa
/ APPLICANT: Hsu, Pei-Ling
/ TITLE OF INVENTION: PRODUCTION OF FUSION PROTEINS AND USE
/ TITLE OF INVENTION: FOR IDENTIFYING BINDING MOLECULES
/ FILE REFERENCE: 13062-002001
/ CURRENT APPLICATION NUMBER: US/10/077,213
/ CURRENT FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: 60/318,474
/ PRIOR FILING DATE: 2001-09-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker sequence
US-10-077-213-4

Query Match      100.0%; Score 66; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SSSSSSSSSSSSSSG 15
Db      1 SSSSSSSSSSSSSSG 15

RESULT 9
US-10-077-210-4
/ Sequence 4, Application US/10077210
/ Publication No. US20030049801A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Chung-Hsiun
/ APPLICANT: Lin, Rong-Hwa
/ APPLICANT: Hsu, Pei-Ling
/ TITLE OF INVENTION: PRODUCTION OF RECOMBINANT PROTEINS IN VIVO AND USE FOR GENERATING
/ TITLE OF INVENTION: ANTIBODIES
/ FILE REFERENCE: 13062-004001
/ CURRENT APPLICATION NUMBER: US/10/077,210
/ CURRENT FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: 60/318,474
/ PRIOR FILING DATE: 2001-09-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Linker sequence
US-10-077-210-4

Query Match      100.0%; Score 66; DB 14; Length 17;
```

Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
|||||
Db 1 SSSSSSSSSSSSSSG 15

RESULT 10

US-10-608-710-9
; Sequence 9, Application US/10608710
; Publication No. US20040117863A1
; GENERAL INFORMATION:
; APPLICANT: CTC Biotherapeutics, Inc.
; APPLICANT: Edge, Michael D
; APPLICANT: Pollock, Daniel
; APPLICANT: Echelard, Yann
; APPLICANT: Meade, Harry M
; APPLICANT: Rybak, Susana M
; TITLE OF INVENTION: Transgenically Produced Fusion Proteins
; FILE REFERENCE: GTC-42D
; CURRENT APPLICATION NUMBER: US/10/608,710
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 09/398,610
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 17
; TYPE: PRT
; ORGANISM: peptide linker
US-10-608-710-9

Query Match 100.0%; Score 66; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
|||||
Db 1 SSSSSSSSSSSSSSG 15

RESULT 11

US-10-768-873-4
; Sequence 4, Application US/10768873
; Publication No. US20040143857A1
; GENERAL INFORMATION:
; APPLICANT: Young, Michael
; APPLICANT: Meade, Harry
; APPLICANT: Krane, Ian
; TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
; FILE REFERENCE: 10275/041001
; CURRENT APPLICATION NUMBER: US/10/768,873
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US/09/333,213
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated linker sequence
US-10-768-873-4

Query Match 100.0%; Score 66; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
|||||
Db 1 SSSSSSSSSSSSSSG 15

RESULT 12

US-09-996-069-12
; Sequence 12, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBIT
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-12

Query Match 100.0%; Score 66; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
|||||
Db 7 SSSSSSSSSSSSSSG 21

RESULT 13

US-10-003-681-1
; Sequence 1, Application US/10003681
; Publication No. US20020156112A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, R. Shoshana
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: ENDOSTATIN-LIKE ANGIOGENESIS INHIBITION
; FILE REFERENCE: M01015-70046-US
; CURRENT APPLICATION NUMBER: US/10/003,681
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,865
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/277,922
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-10-003-681-1

Query Match 100.0%; Score 66; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
|||||
Db 7 SSSSSSSSSSSSSSG 21

RESULT 14

US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; Houston, L. L.

Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
IMAGING
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teeter, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 100.0%; Score 66; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSGSSSG 15
|||
Db 118 SSSSGSSSSGSSSG 132

RESULT 15
US-10-683-547-6
Sequence 6, Application US/10683547
Publication No. US20050058638A1
GENERAL INFORMATION:
APPLICANT: Houston, J.
APPLICANT: Houston, L.L.
APPLICANT: Ring, D.
APPLICANT: Oppermann, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
FILE REFERENCE: CIBT-P01-130
CURRENT APPLICATION NUMBER: US/10/683,547
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 07/831,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 520C9 gfv

US-10-683-547-6
Query Match 100.0%; Score 66; DB 17; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSGSSSSGSSSG 15
|||
Db 118 SSSSGSSSSGSSSG 132

Search completed: April 4, 2005, 16:42:47
Job time : 23.1406 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:32:36 ; Search time 5.41534 seconds
(without alignments)
266.512 Million cell updates/sec

Title: US-09-887-853-8
Perfect score: 66
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 60 | 90.9 | 304 | 2 | T16535 |
| 2 | 57 | 86.4 | 1249 | 2 | T26294 |
| 3 | 57 | 86.4 | 1751 | 2 | A45604 |
| 4 | 56 | 84.8 | 683 | 2 | A82704 |
| 5 | 54 | 81.8 | 107 | 2 | B85356 |
| 6 | 54 | 81.8 | 162 | 2 | C85356 |
| 7 | 54 | 81.8 | 406 | 2 | S38170 |
| 8 | 54 | 81.8 | 424 | 2 | T08093 |
| 9 | 54 | 81.8 | 475 | 2 | S49886 |
| 10 | 54 | 81.8 | 623 | 1 | S31167 |
| 11 | 54 | 81.8 | 679 | 2 | AC0333 |
| 12 | 54 | 81.8 | 1215 | 2 | I52882 |
| 13 | 54 | 81.8 | 1791 | 2 | T02345 |
| 14 | 54 | 81.8 | 1912 | 2 | T29088 |
| 15 | 52 | 78.8 | 284 | 2 | A35419 |
| 16 | 52 | 78.8 | 419 | 2 | D83465 |
| 17 | 51 | 77.3 | 153 | 2 | S67294 |
| 18 | 51 | 77.3 | 270 | 2 | F86177 |
| 19 | 51 | 77.3 | 286 | 2 | A34615 |
| 20 | 51 | 77.3 | 299 | 2 | T12483 |
| 21 | 51 | 77.3 | 447 | 2 | E83465 |
| 22 | 51 | 77.3 | 456 | 2 | S69070 |
| 23 | 51 | 77.3 | 562 | 2 | B41035 |
| 24 | 51 | 77.3 | 562 | 2 | S50371 |
| 25 | 51 | 77.3 | 750 | 2 | T04980 |
| 26 | 51 | 77.3 | 825 | 1 | EDBEXD |
| 27 | 51 | 77.3 | 1677 | 2 | T43021 |
| 28 | 50 | 75.8 | 218 | 2 | JC7220 |
| 29 | 50 | 75.8 | 335 | 2 | T14449 |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 30 | 50 | 75.8 | 380 | 2 | T14447 | oleosin homolog pc |
| 31 | 50 | 75.8 | 419 | 2 | T14448 | oleosin homolog pc |
| 32 | 50 | 75.8 | 440 | 2 | S37303 | box-4 protein - mo |
| 33 | 50 | 75.8 | 559 | 1 | RWBYS1 | glycophospholipid- |
| 34 | 50 | 75.8 | 625 | 2 | T41603 | alpha-amylose - fl |
| 35 | 50 | 75.8 | 710 | 2 | S28014 | outd protein - Erw |
| 36 | 50 | 75.8 | 712 | 2 | B47021 | pectic enzyme secr |
| 37 | 50 | 75.8 | 741 | 2 | I48694 | probable transcrip |
| 38 | 50 | 75.8 | 742 | 2 | A49672 | transcription fact |
| 39 | 50 | 75.8 | 772 | 2 | A55004 | transcription fact |
| 40 | 50 | 75.8 | 1029 | 2 | T30351 | mucin-like protein |
| 41 | 50 | 75.8 | 1446 | 1 | A45344 | immediate-early pr |
| 42 | 50 | 75.8 | 1460 | 1 | EDBEIF | immediate-early pr |
| 43 | 50 | 75.8 | 1723 | 2 | H66557 | polymorphic membra |
| 44 | 50 | 75.8 | 1723 | 2 | E72067 | polymorphic membra |
| 45 | 50 | 75.8 | 1732 | 2 | C81601 | polymorphic membra |

ALIGNMENTS

RESULT 1
T16535
hypothetical protein K02F3.11 - Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: T16535
R/Bentley, D.
Submitted to the EMBL Data Library, May 1994
A/Description: The sequence of C. elegans cosmid K02F3.
A/Reference number: Z18530
A/Accession: T16535
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-304 <BEN>
A/Cross-references: EMBL:U00052; NID:9485125; PID:9485126; PIDN:AAA50702.1; CESP:K02F3.11
C/Genetics:
A/Experimental source: strain Bristol N2
A/Reference number: Z20191
A/Accession: T26294
R/Lloyd, C.
Submitted to the EMBL Data Library, December 1995
A/Reference number: Z20191
A/Accession: T26294
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1249 <WIL>
A/Cross-references: EMBL:Z68221; PIDN:CAA92495.1; GSPDB:GN00022; CESP:W09C2.3
A/Experimental source: clone W09C2
C/Genetics:
A/Map position: 4
A/Introns: 32/3; 58/3; 117/3; 211/3; 263/3; 675/3; 1139/3; 1187/1; 1230/3
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain <ATN>
P/700-885/Domain: ATPase nucleotide-binding domain homology <ATN>

| | | | | |
|---|-----------------|-------------------|-----------|--------------|
| Query Match | 90.9%; | Score 60; | DB 2; | Length 304; |
| Best Local Similarity | 93.3%; | Pred. No. 0.98; | | |
| Matches 14; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 1 | SSSSSSSSSSSSSG 15 | | |
| DB | 14 | SSSSSSSSSSSSSG 28 | | |
| RESULT 2 | | | | |
| T26294 | | | | |
| hypothetical protein W09C2.3 - Caenorhabditis elegans | | | | |
| C/Species: Caenorhabditis elegans | | | | |
| C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2000 | | | | |
| A/Accession: T26294 | | | | |
| A/Reference number: Z20191 | | | | |
| A/Status: preliminary; translated from GB/EMBL/DBJ | | | | |
| A/Molecule type: DNA | | | | |
| A/Residues: 1-1249 <WIL> | | | | |
| A/Cross-references: EMBL:Z68221; PIDN:CAA92495.1; GSPDB:GN00022; CESP:W09C2.3 | | | | |
| A/Experimental source: clone W09C2 | | | | |
| C/Genetics: | | | | |
| A/Map position: 4 | | | | |
| A/Introns: 32/3; 58/3; 117/3; 211/3; 263/3; 675/3; 1139/3; 1187/1; 1230/3 | | | | |
| C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain <ATN> | | | | |
| P/700-885/Domain: ATPase nucleotide-binding domain homology <ATN> | | | | |
| Query Match | 86.4%; | Score 57; | DB 2; | Length 1249; |

A:Accession: S38170
 A:Molecule type: DNA
 A:Residues: 1-406 <BAL>
 A:Cross-references: UNIPROT:P32583; EMBL:Z28317; NID:g486580; PID:g486581; MIPS:YKR092c
 A:Experimental source: strain S288C
 R:Bou, G.; Batean, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji
 Yeast 9, 1349-1354, 1993
 A>Title: The complete sequence of a 15 820 bp segment of *Saccharomyces cerevisiae* chromo
 A:Reference number: S40644; MUID:94205265; PMID:8154186
 A:Accession: S40645
 A:Molecule type: DNA
 A:Residues: 1-406 <BOU>
 A:Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51946.1; PID:g450552
 A:Experimental source: strain S288C
 R:Liao, D.; Carles, C.; Sentenac, A.; Thuriaux, P.
 Submitted to the EMBL Data Library, May 1993
 A:Description: Interactions between three common subunits of yeast RNA polymerases I and
 A:Reference number: S37702
 A:Accession: S37702
 A:Molecule type: DNA
 A:Residues: 1-399,'N',401-406 <LAL>
 A:Cross-references: EMBL:L1275; NID:g295670; PID:g295671
 C:Genetics:
 A:Gene: SGD:SRP40
 A:Cross-references: SGD:S0001800; MIPS:YKR092c
 A:Map position: 11R

Query Match 81.8%; Score 54; DB 2; Length 406;
 Best Local Similarity 92.9%; Pred. No. 6.9;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSSGSSSSSSSSSS 14
 |||||
 Db 100 SSSGSSSSSSSSSS 113

RESULT 8

T08093
 oleosin homolog STA 41-2 - rape
 C:Species: *Brassica napus* (rape)
 C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C:Accession: T08093
 R:Robert, L.S.; Gerslter, J.; Allard, S.; Cass, L.; Simmonds, J.
 Plant J. 6, 927-933, 1994
 A>Title: Molecular characterization of two *Brassica napus* genes related to oleosins whic
 A:Reference number: Z16348; MUID:95152562; PMID:7849761
 A:Accession: T08093
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-424 <ROB>
 A:Cross-references: UNIPROT:Q42626; EMBL:I33282; NID:g495010; PIDN:AAA70400.1; PID:g9042
 A:Experimental source: cv. Westar; tapetum
 A>Note: protein component of lipid storage bodies of plants
 C:Genetics:
 A:Gene: STA 41-2

Query Match 81.8%; Score 54; DB 2; Length 424;
 Best Local Similarity 80.0%; Pred. No. 7.2;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSSGSSSSSSSSSSG 15
 |||||
 Db 400 SSSGSSSSSSSSSDG 414

RESULT 9

S49886
 probable membrane protein YII123w - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: hypothetical protein Y18277.06
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S49886
 R:Hamlyn, N.; Churcher, C.

submitted to the EMBL Data Library, November 1994
 A:Reference number: S49881
 A:Accession: S49886
 A:Molecule type: DNA
 A:Residues: 1-475 <HAN>
 A:Cross-references: UNIPROT:P40472; GB:Z47047; EMBL:Z46833; NID:g603997; PID:g763223; MI
 C:Genetics:
 A:Gene: SGD:SIM1
 A:Cross-references: SGD:S0001385; MIPS:YII123w
 A:Map position: 9L
 C:Superfamily: *Saccharomyces* NCA3 protein
 C:Keywords: transmembrane protein
 F:82-98/Domain: transmembrane #status predicted <TM>

Query Match 81.8%; Score 54; DB 2; Length 475;
 Best Local Similarity 86.7%; Pred. No. 8;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSSGSSSSSSSSSSG 15
 |||||
 Db 186 SSSGSSSSSSSSSSG 200

RESULT 10

S33167
 gene pointed protein splice form 1 - fruit fly (*Drosophila melanogaster*)
 N/Alternate names: ETS-like protein
 C:Species: *Drosophila melanogaster*
 C>Date: 13-Jan-1995 #sequence_revision 30-May-1997 #text_change 09-Jul-2004
 C:Accession: S33167; S28819; S28818
 R:Klaemdt, C.
 Development 117, 163-176, 1993

A>Title: The *Drosophila* gene pointed encodes two ETS-like proteins which are involved in
 A:Reference number: S33167; MUID:94038653; PMID:8232245
 A:Accession: S33167
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-623 <KLA>
 A:Cross-references: UNIPROT:P51022; EMBL:X69166; NID:g288079; PIDN:CAA48916.1; PID:g28808
 R:Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
 Dev. Biol. 151, 176-191, 1992

A>Title: Isolation and characterization of five *Drosophila* genes that encode an ets-relat
 A:Reference number: S28819; MUID:92249640; PMID:1577186
 A:Accession: S28819
 A:Molecule type: mRNA

A:Residues: 456-613 <CHE>
 A:Cross-references: EMBL:M88472; NID:g157191; PIDN:AAC34200.1; PID:g157192
 R:Pihyl, L.J.; Watson, D.K.; McWilliams, M.J.; Ascione, R.; Papas, T.S.
 Dev. Biol. 127, 45-53, 1988

A>Title: The *Drosophila* ets-2 gene: molecular structure, chromosomal localization, and de
 A:Reference number: S28818; MUID:88196618; PMID:2834248
 A:Accession: S28818
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 445-466,'R',468-603 <PRI>
 A:Cross-references: EMBL:M20408; NID:g157384; PIDN:AAA28521.1; PID:g157385
 A>Note: the authors translated the codon AGA for residue 467 as Gin
 C:Genetics:

A:Gene: FlyBase:pnt
 A:Cross-references: FlyBase:FBgn0003118
 A:Introns: 550/3

C:Superfamily: pointed protein, splice form 1; ets DNA-binding domain homology
 C:Keywords: alternative splicing; DNA binding; nucleus; transcription factor
 F:517-595/Domain: ets DNA-binding domain homology <BTS>

Query Match 81.8%; Score 54; DB 1; Length 623;
 Best Local Similarity 85.7%; Pred. No. 10;
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGSSSSSSSSSS 14
 ::|||
 Db 158 TTSSGSSSSSSSSSS 171

RESULT 11
AC0333
Probable membrane protein YP02731 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC0333
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AC0333
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-679 <KIR>
A/Cross-references: UNIPROT:Q8ZD61; GB:AL590842; PIDD:CA92970.1; PID:g15980709; GSPDB:C/Genetics:
A/Gene: YP02731

Query Match 81.8%; Score 54; DB 2; Length 679;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15
Db 654 SSSSGSSSGSSSG 668

RESULT 12
152882
antigen - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 152882
R/Bloch, D.B.; Rabkina, D.; Quertermous, T.; Bloch, K.D.
Clin. Immunol. Immunopathol. 72, 380-389, 1994
A/Title: The immunoreactive region in a novel autoantigen contains a nuclear localization
A/Reference number: 152882; MUID:4340813; PMID:7550377
A/Accession: 152882
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1215 <RES>
A/Cross-references: UNIPROT:Q13826; GB:L26339; NID:g533201; PIDD:AAA21833.1; PID:g533202
C/Superfamily: human autoantigen Ge-1

Query Match 81.8%; Score 54; DB 2; Length 1215;
Best Local Similarity 92.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 14
Db 614 SSSSGSSSGSSSG 627

RESULT 13
T02345
hypothetical protein KIAA0324 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02345
R/Ricke, D.O.; Bruce, D.; Muntz, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.; re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.
submitted to the EMBL Data Library, March 1998
A/Description: Sequencing of human chromosome 16p13.3.
A/Reference number: Z14664
A/Accession: T02345
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1791 <RIC>
A/Cross-references: UNIPROT:O60382; EMBL:AC004493; NID:g2996648; PIDD:AAC08453.1; PID:g2
C/Genetics:

A/Map position: 16
A/Introns: 1610/2; 1706/2
A/Note: KIAA0324

Query Match 81.8%; Score 54; DB 2; Length 1791;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 15
Db 1575 SSSSGSSSGSSSG 1589

RESULT 14
T29088
vitellogenin I precursor [validated] - chicken
N/containing: lipovitellin I; lipovitellin II; phosvitin; yolk glycoprotein 42K
C/Species: Gallus gallus (chicken)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29088; S55681
R/Mabuchi, N.; Yamamura, J.; Adachi, T.; Aoki, N.; Nakamura, R.; Matsuda, T.
submitted to the EMBL Data Library, November 1996
A/Description: cDNA cloning and estrogen-induced expression of chicken vitellogenin I.
A/Reference number: Z20557
A/Accession: T29088
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1912 <MAB>
A/Cross-references: UNIPROT:P87498; EMBL:D89547; PIDD:BA13973.1
A/Experimental source: liver
R/Yamamura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1244, 384-394, 1995
A/Title: Precursor-product relationship between chicken vitellogenin and the yolk protein

A/Reference number: S55680; MUID:95322425; PMID:7599159
A/Accession: S55681
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1628-1639 <YAM>
C/Superfamily: vitellogenin
C/Keywords: egg yolk; glycoprotein; liver; phosphoprotein
F/1-15/Domain: signal sequence #status predicted <SIG>
F/16-1912/Product: vitellogenin I #status predicted <MAB>

Query Match 81.8%; Score 54; DB 2; Length 1912;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSSGSSSGSSSG 14
Db 1150 SSSSGSSSGSSSG 1163

RESULT 15
A35419
neutrophil protein - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C/Accession: A35419
R/Bellavite, P.; Bazzoni, F.; Cassatella, M.A.; Hunter, K.J.; Bannister, J.V.
Biochem. Biophys. Res. Commun. 170, 915-922, 1990
A/Title: Isolation and characterization of a cDNA clone for a novel serine-rich neutrophil
A/Reference number: A35419; MUID:90343818; PMID:1656479
A/Accession: A35419
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-284 <BEL>
A/Cross-references: UNIPROT:Q99331; GB:M55701; NID:g164672; PIDD:AAA63449.1; PID:g164673

Query Match 78.8%; Score 52; DB 2; Length 284;
Best Local Similarity 86.7%; Pred. No. 8.6;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSSSSSSSSSSSSSG 15
| | | | |
Db 146 SSSSSSSSSSTSSSG 160

Search completed: April 4, 2005, 15:58:06
Job time : 6.41534 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 4, 2005, 15:20:59 ; Search time 25.3514 seconds
(without alignments)
302.988 Million cell updates/sec

Title: US-09-887-853-8
Perfect score: 66
Sequence: 1 SSSSSSSSSSSSSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 66 | 100.0 | 192 | 2 | Q7YY80 | cryptospori |
| 2 | 66 | 100.0 | 289 | 2 | Q21155 | caenorhabd |
| 3 | 66 | 100.0 | 453 | 2 | Q6C6N1 | Q6C6N1 yarrowia 11 |
| 4 | 60 | 90.9 | 368 | 2 | Q6WNT4 | Q6WNT4 fugu rubrip |
| 5 | 60 | 90.9 | 1357 | 2 | Q9W4M4 | Q9W4M4 drosophila |
| 6 | 59 | 89.4 | 218 | 2 | Q759N0 | Q759N0 ashbya gose |
| 7 | 59 | 89.4 | 619 | 2 | Q7PQ47 | Q7PQ47 anopheles g |
| 8 | 58 | 87.9 | 394 | 2 | Q8T010 | Q8T010 methanobarc |
| 9 | 58 | 87.9 | 525 | 2 | Q693B7 | Q693B7 microbulbit |
| 10 | 58 | 87.9 | 1124 | 2 | Q7QDA9 | Q7QDA9 anopheles g |
| 11 | 57 | 86.4 | 300 | 2 | Q86JX6 | Q86JX6 dictyostel |
| 12 | 57 | 86.4 | 303 | 2 | Q95VT3 | Q95VT3 dictyostel |
| 13 | 57 | 86.4 | 419 | 2 | Q9W9E1 | Q9W9E1 drosophila |
| 14 | 57 | 86.4 | 694 | 2 | Q9CS92 | Q9CS92 mus musculu |
| 15 | 57 | 86.4 | 1228 | 2 | Q45215 | Q45215 caenorhabd |
| 16 | 57 | 86.4 | 1249 | 2 | Q6T363 | Q6T363 caenorhabd |
| 17 | 57 | 86.4 | 1352 | 2 | Q6T364 | Q6T364 caenorhabd |
| 18 | 57 | 86.4 | 1388 | 2 | Q69363 | Q69363 feline hepr |
| 19 | 57 | 86.4 | 1403 | 2 | Q9VPO4 | Q9VPO4 drosophila |
| 20 | 57 | 86.4 | 1488 | 2 | Q86B57 | Q86B57 drosophila |
| 21 | 57 | 86.4 | 1751 | 2 | Q26194 | Q26194 plameodim |
| 22 | 56 | 84.8 | 367 | 2 | Q86K15 | Q86K15 dictyostel |
| 23 | 56 | 84.8 | 400 | 1 | RTOA_DICDI | P54681 dictyostel |
| 24 | 56 | 84.8 | 477 | 2 | Q9FGM9 | Q9FGM9 arabidopsis |
| 25 | 56 | 84.8 | 544 | 2 | Q54802 | Q54802 mus musculu |
| 26 | 56 | 84.8 | 544 | 2 | Q794H2 | Q794H2 mus sp. mb2 |
| 27 | 56 | 84.8 | 590 | 2 | Q693B6 | Q693B6 microbulbit |
| 28 | 56 | 84.8 | 683 | 2 | Q9PDW2 | Q9PDW2 xylella fas |
| 29 | 56 | 84.8 | 773 | 2 | P79149 | P79149 canis famli |
| 30 | 55 | 83.3 | 283 | 2 | Q6NZV7 | Q6NZV7 brachydanio |
| 31 | 55 | 83.3 | 283 | 2 | Q6PG31 | Q6PG31 brachydanio |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 32 | 55 | 83.3 | 332 | 2 | Q6C1Z7 | Q6C1Z7 yarrowia 11 |
| 33 | 55 | 83.3 | 410 | 2 | Q7S340 | Q7S340 neurospora |
| 34 | 54 | 81.8 | 69 | 2 | Q86JX8 | Q86JX8 dictyostel |
| 35 | 54 | 81.8 | 90 | 2 | Q7RWL2 | Q7RWL2 neurospora |
| 36 | 54 | 81.8 | 107 | 2 | Q9M0B5 | Q9M0B5 arabidopsis |
| 37 | 54 | 81.8 | 149 | 2 | Q8CSW6 | Q8CSW6 mus musculu |
| 38 | 54 | 81.8 | 162 | 2 | Q6BD40 | Q6BD40 drosophila |
| 39 | 54 | 81.8 | 162 | 2 | Q9M0B4 | Q9M0B4 arabidopsis |
| 40 | 54 | 81.8 | 167 | 2 | Q6EP11 | Q6EP11 oryza sativ |
| 41 | 54 | 81.8 | 202 | 2 | Q9V760 | Q9V760 drosophila |
| 42 | 54 | 81.8 | 203 | 2 | Q8WMA1 | Q8WMA1 homo sapien |
| 43 | 54 | 81.8 | 203 | 2 | Q9NUZ4 | Q9NUZ4 homo sapien |
| 44 | 54 | 81.8 | 256 | 2 | Q82F25 | Q82F25 streptomyce |
| 45 | 54 | 81.8 | 266 | 2 | Q9H0J0 | Q9H0J0 homo sapien |

ALIGNMENTS

RESULT 1
Q7YY80 PRELIMINARY; PRT; 192 AA.
AC Q7YY80;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Serine repeat antigen, probable.
GN ORFNames=56k.04;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
RT "Integrated mapping, chromosomal sequencing and sequence analysis of
RT Cryptosporidium parvum.";
RL Genome Res. 0:0-0(2003).
DR EMBL; BX536350; CAD98606.1; -.
SQ SEQUENCE 192 AA; 19686 MW; CB363BP9B40F77 CRC64;

Query Match 100.0%; Score 66; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSSSSSSSSSSSSSG 15
Db 155 SSSSSSSSSSSSSSG 169
(1)

RESULT 2
ID Q21155 PRELIMINARY; PRT; 289 AA.
AC Q21155;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-2002 (TREMBlrel. 20, Last sequence update)
DT 01-NOV-2004 (TREMBlrel. 26, Last annotation update)
DE Rnp (Rnm rna binding domain) containing protein 5.
GN Name-rnp-5; ORFNames=K02F3.11;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG Wormbase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]

```

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid K02F3."
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA WormBase Consortium;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: U00052; AKK21429.2; -.
DR WormBase: WBGene00004388; rnp-5.
DR WormPep: K02F3.11; CE29981.
DR InterPro: IPR00504; RNA_rec_mot.
DR Pfam: PF00076; RRM_1; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS00102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 289 AA; 3237 MW; CFE82B8BD2E230E CRC64;

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Query Match          100.0%; Score 66; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSG 15
DB 19 SSSSSSSSSSSSSSG 33

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RESULT 3

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ID O6C6N1 PRELIMINARY; PRT; 453 AA.
AC O6C6N1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DB Similar to tr|008294 Saccharomyces cerevisiae Y01J55C.
GN ORFNames=YAL105080089;
OS Yarrowia lipolytica CL1B99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RG Genolevures;
RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugebisse C., Talla B.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Cactolico L., Contandoli F., de Darivar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
RA Hantraye F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Witth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,

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RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR382131; CAG792270.1; -.
SQ SEQUENCE 453 AA; 43707 MW; 097090FA7AE15F50 CRC64;

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```

Query Match          100.0%; Score 66; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSSSSSSSSSSSSSG 15
DB 341 SSSSSSSSSSSSSSG 355

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RESULT 4

```

ID O6WNT4 PRELIMINARY; PRT; 368 AA.
AC O6WNT4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transcription factor Sox11.
GN Name=Sox11;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed:15019997; DOI=10.1016/j.gene.2003.12.008;
RA Koopman P., Schepers G., Brenner S., Venkatesh B.;
RT "Origin and diversity of the SOX transcription factor gene family:
RT genome-wide analysis in Fugu rubripes."
RL Gene 328:177-186(2004).
DR EMBL: AY277959; AAC18502.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR009071; HMG-box.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00505; HMG_box; 1.
DR SMART: SM00398; HMG; 1.
DR PROSITE: PS00118; HMG_BOX_2; 1.
SQ SEQUENCE 368 AA; 40719 MW; ECF81ED074EFD7 CRC64;

```

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Query Match          90.9%; Score 60; DB 2; Length 368;
Best Local Similarity 93.3%; Pred. No. 6.8;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 SSSSSSSSSSSSSSG 15
DB 272 SSSSSSSSSSSSSSG 286

```

RESULT 5

```

ID O9W4M4 PRELIMINARY; PRT; 1357 AA.
AC O9W4M4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG15570-PA.
GN ORFNames=CG15570;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```


OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gockyne U.D.,
RA Amanaidee P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazaj R.G., Chape M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Agbayan A., An H.J., Andrews-Pitmanoch C., Baldwin D.,
RA Ballew R.M., Baau A.A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bens P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Bokkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cateley S., Dahle C., Davenport L.B., Davies F.,
RA de Palois B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dunbar K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Foster C., Gabriellian A.E., Garg N.S., Galbraith W.M., Glaeser K.,
RA Glodet A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegami C.,
RA Jajal M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacel J.M.,
RA Palazzolo M., Plington G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.E., Smith T.,
RA Spraker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svayres R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Weasman D.A., Weinstein G.G., Wu D., Weisenbach J.,
RA Williams S.M., Woodagel, Morley K.C., Mu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champ M., Dugan S.P., Fife E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svayres R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G.G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RL *melanogaster* euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Celniker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svayres R.,
RA Patel S., Fife E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatic
RL genome perspective.";
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Celniker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
RA Bettecourt C.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

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| RA | Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; |
| RA | "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review"; |
| RT | Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002). |
| RN | [5] |
| RP | SEQUENCE FROM N.A. |
| RG | FlyBase; |
| RL | Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. |
| RN | [6] |
| RP | SEQUENCE FROM N.A. |
| RG | FlyBase; |
| RL | Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. |
| DR | EMBL; AE003430; AAF45927.1; -. |
| DR | FlyBase; FBgn0029697; CG15570. |
| SQ | SEQUENCE 1357 AA; 136890 MW; C282DC86FE34A61A CRC64; |
| OY | 1 SSSSGSSSSGSSSS 14 |
| Db | 563 SSSSGSSSSGSSSS 576 |
| Query Match | 90.9%; Score 60; DB 2; Length 1357; |
| Best Local Similarity | 100.0%; Pred. No. 27; |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| RESULT 6 | |
| O759NO | PRELIMINARY; PRT; 218 AA. |
| AC O759NO; | |
| DT 05-JUL-2004 (TREMBLrel. 27, Created) | |
| DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update) | |
| DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update) | |
| DE AD8246CD. | |
| CN ORFNames=ADR246C; | |
| OS Ashdya gossypii (Yeast) (Eremothecium gossypii). | |
| OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | |
| OC Saccharomycetales; Saccharomycetaceae; Eremothecium. | |
| OX NCBI_TaxID=33169; | |
| RN [1] | |
| RN RN | SEQUENCE FROM N.A. |
| RC STRAIN=ATCC 10895; | |
| RA Voegelé S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T., Philippsen P.; | |
| RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. | |
| DR EMBL; AE016817; AAS52166.1; -. | |
| DR AGD; ADR246C; -. | |
| SQ SEQUENCE 218 AA; 19346 MW; 7B5103FD1B0BC52 CRC64; | |
| Query Match | 89.4%; Score 59; DB 2; Length 218; |
| Best Local Similarity | 86.7%; Pred. No. 5.1; |
| Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0; | |
| OY 1 SSSSGSSSSGSSSSG 15 | |
| Db 167 SSSSGSSSETGSSGS 181 | |
| RESULT 7 | |
| O7PQ47 | PRELIMINARY; PRT; 619 AA. |
| AC O7PQ47; | |
| DT 01-MAR-2004 (TREMBLrel. 26, Created) | |
| DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update) | |
| DT ENSANGP0000021699 (Fragment). | |
| CN Name=ENSANGG0000019210; | |
| OS Anopheles gambiae str. PE87. | |
| OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota; | |
| OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles. | |
| OX NCBI_TaxID=180454; | |
| RN [1] | |
| RP SEQUENCE FROM N.A. | |

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RC STRAIN-PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008900; EAA09315.2; -.
FT NON_TER 1 619 619
SQ SEQUENCE 619 AA; 60241 MW; 3A74385560D44E93 CRC64;

Query Match
Best Local Similarity 89.4%; Score 59; DB 2; Length 619;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSGSSSSSSSSSSSG 15
DB 222 SSSGSSSSSSSSSSSG 236

RESULT 8
O8T0L0 PRELIMINARY; PRT; 394 AA.
ID O8T0L0
AC O8T0L0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein MA1742.
GN OrderedlocusNames=MA1742;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-G2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929780; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thoman N., Dearlilano K., Johnson R.,
RA Lincon L., McEwan P., McKernan K., Talama J., Turrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner B.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umyam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010848; AAM05149.1; -.
DR InterPro; IPR008962; Papd-1like.
KW Complete proteome.
SQ SEQUENCE 394 AA; 42431 MW; 1D2C7304B147D6B CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 394;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSSGSSSSSSSSSSSG 15
DB 132 SSSGSSSSSSSSSSSG 145

RESULT 9
O693B7 PRELIMINARY; PRT; 525 AA.
ID O693B7;
AC O693B7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Endo-chitinase.

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GN Name=chIB;
OS Microbubifer hydrolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Microbubifer.
OX NCBI_TaxID=48074;
RN [1]
RP SEQUENCE FROM N.A.
RA Howard M.B., Ekborg N.A., Taylor L.E. Jr., Weiner R.M.,
RA Hutcheson S.W.;
RT "Complex polysaccharide metabolic profiles of Microbubifer sp. and
RT analysis of chitinases and other degradative enzymes of Microbubifer
RT hydrolyticus.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646087; AAT61213.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0030246; F:carbohydrate binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003610; CEM_5_12.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF02839; CEM_5_12; 2.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00495; ChbD3; 2.
DR PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
KW Glycosidase; Hydrolyase.
SQ SEQUENCE 525 AA; 53761 MW; 3794374935464EA9 CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 525;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSGSSSSSSSSSSSG 15
DB 192 SSSGSSSSSSSSSSSG 206

RESULT 10
O70DA9 PRELIMINARY; PRT; 1124 AA.
ID O70DA9
AC O70DA9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AgCP1543.
GN Name=agCG55963; ORFNames=ENSNANG0000015740;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Cullcoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAA07880.1; -.
DR InterPro; IPR002553; Adaptin_N.
DR InterPro; IPR008938; ARM.
DR Pfam; PF01602; Adaptin_N; 1.
SQ SEQUENCE 1124 AA; 122427 MW; 06332B0FCB5AD1F4 CRC64;

Query Match
Best Local Similarity 87.9%; Score 58; DB 2; Length 1124;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSSGSSSSSSSSSSSG 15
DB 736 SSSGSSSSSSSSSSSG 749

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RESULT 11
086JX6 PRELIMINARY; PRT; 300 AA.
ID 086JX6;
AC 086JX6;
DT 01-JUN-2003 (TREMBLrel. 24, Last Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Similar to Dictyostelium discoideum (Slime mold). CF50.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachbat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; NA051376.1; -.
DR DictyBase; DDB0185090; CF50.
DR GO; GO:0003796; P:lysozyme activity; IEA.
DR GO; GO:0016988; P:cell wall catabolism; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002053; Glyco_hydro_25; 1.
DR ProDom; PD004620; Glyco_hydro_25; 1.
SQ SEQUENCE 300 AA; 30480 MW; FAEBB7A6D967467 CRC64;

Query Match 86.4%; Score 57; DB 2; Length 300;
Beet Local Similarity 80.0%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSSSSSSSSSSSSG 15
DB 254 SSSSSSSSSSSSSSG 268

RESULT 12
095VT3 PRELIMINARY; PRT; 303 AA.
ID 095VT3;
AC 095VT3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE CF50.
GN Name=CF50;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22112679; PubMed=12117815;
RA Brock D.A., Hatton R.D., Giurgutiu D.V., Scott B., Ammann R.,
RA Gomer R.H.;
RT "The different components of a multistep cell number-counting
RT factor have both unique and overlapping functions.";
RL Development 129:3657-3668(2002).
DR EMBL; AF405695; AL01036.1; -.
DR DictyBase; DDB0185090; CF50.
SQ SEQUENCE 303 AA; 30854 MW; 2B2A3CC1CEB3CE8A CRC64;

Query Match 86.4%; Score 57; DB 2; Length 303;
Beet Local Similarity 80.0%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SSSSSSSSSSSSSSG 15
DB 257 SSSSSSSSSSSSSSG 271

RESULT 13
09VW91 PRELIMINARY; PRT; 419 AA.
ID 09VW91;
AC 09VW91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE CG7290-PA (R65123p).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abrial J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benes P.V., Bertan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Folsler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hootin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod W.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spindling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskay R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA Patel R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svitskay R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
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RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Friese B., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
RA Bencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Lao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phoumenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RX EMBL; AEO03514; AAF49058.3; -
RX EMBL; AY071500; AAL49222.1; -
DR InChit; O9VM91; -
DR FlyBase; FBgn0036949; CG7290.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM_14; 5.
DR SMART; SM00494; ChtBD2; 5.
DR PROSITE; PS50940; CHIT_BIND_II; 5.
DR SEQUENCE 419 AA; 42406 MW; DE8E397DD009DF2 CRC64;
SQ

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Warahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Arai A., Kono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RX EMBL; AK017507; BAB30779.2; -
DR MGD; MGI:1913875; 5730406M06Rik.
DR Hypothetical protein.
KW NON TER
FT
SQ SEQUENCE 694 AA; 79382 MW; 699D6A63F6A07D0D CRC64;

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Query Match 86.4%; Score 57; DB 2; Length 419;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Query Match 86.4%; Score 57; DB 2; Length 694;
Best Local Similarity 92.9%; Pred. No. 31;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 508 SSSSSSSSSSSSG 521

RESULT 15

ID 045215 PRELIMINARY; PRT: 1228 AA.
 AC 045215;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Calcium ATPase.
 GN Name=mca-1; ORFNames=M09C2.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodertinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB1489 him-8;
 RX MEDLINE=99134356; PubMed=9933625; DOI=10.1074/jbc.274.7.4254;
 RA Kraev A., Kraev N., Carafoli E.;
 RT "Identification and functional expression of the plasma membrane
 calcium ATPase gene family from Caenorhabditis elegans.";
 RL J. Biol. Chem. 274:4254-4258(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB1489 him-8;
 RA Kraev A.S.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 EMBL: AJ223616; CAU1491.1;
 DR GO:0016021; C:Integral to membrane; IEA.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0005509; F:calcium ion binding; IEA.
 DR GO:0005388; F:calcium-transporting ATPase activity; IEA.
 DR GO:0016787; F:hydrolyase activity; IEA.
 DR GO:0016820; F:hydrolyase activity, acting on acid anhydrid. . .; IEA.
 DR GO:0006816; F:calcium ion transport; IEA.
 DR GO:0006812; F:calcium transport; IEA.
 DR GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR006408; ATPase-IB Ca.
 DR InterPro: IPR01757; ATPase_EI-E2.
 DR InterPro: IPR006068; Cation_ATPase_C.
 DR InterPro: IPR04014; Cation_ATPase_N.
 DR InterPro: IPR005834; Dehal_like_hydro.
 DR Pfam: PF00689; Cation_ATPase_C; 1.
 DR Pfam: PF00690; Cation_ATPase_N; 1.
 DR Pfam: PF01222; EI-E2_ATPase; 1.
 DR Pfam: PF00702; Hydrolyase; 1.
 DR PRINTS: PR00119; CATATPASE.
 DR TIGRFAMs: TIGR01517; ATPase-IB Ca; 1.
 DR TIGRFAMs: TIGR01494; ATPase_P-type; 3.
 DR PROSITE: PS00154; ATPASE_EI-E2; UNKNOWN 1.
 SQ SEQUENCE 1228 AA; 134552 MW; 1F790DFEBBA6108 CRC64;

OY 1 SSSSSSSSSSSSG 15
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 DB 314 SSSSSSSSSSSSG 328

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